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=> fil hcaplus
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FILE COVERS 1907 - 13 Feb 2003  VOL 138 ISS 7
FILE LAST UPDATED: 12 Feb 2003  (20030212/ED)

  This file contains CAS Registry Numbers for easy and accurate
  substance identification.


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L3            38 SEA FILE=REGISTRY ABB=ON  PLU=ON  W{GAILVSTR}{GAILVSTR}WHF/SQSP

L5             1 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L1
L7            27 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L3
L8             1 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L7 AND L4


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L7   ANSWER 1 OF 1  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         2000:686163  HCAPLUS
DOCUMENT NUMBER:          133:145915
TITLE:                    Transcription factor E2F DNA-binding domain inhibiter
                          peptides and uses thereof
INVENTOR(S):              Muller, Rolf; Kontermann, Roland Ernst; Montigiani,
                          Silvia
PATENT ASSIGNEE(S):       Prolifix Limited, UK
SOURCE:                   PCT Int. Appl., 42 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

      PATENT NO.         KIND  DATE          APPLICATION NO.  DATE
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      WO [illegible]     A1    [illegible]   WO [illegible]   [illegible]
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              CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
              IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
              MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
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RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

CA 2389143 AA 20010726 CA 2001-2389143 20010126

EP 1144443 A1 20011017 EP 2001-902228 20010126

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

US 20030013108 A1 20030116 US 2001-811414 20010316

PRIORITY APPLN. INFO.: GB 1999-1710 A 19990126

WO 2000-GB227 W 20000126

OTHER SOURCE(S): MARPAT 139:145915

AB The present invention provides sequences of peptides which bind to the DNA binding domain of transcription factor E2F, and inhibit cell cycle progression. Peptides include FWLRFT, WVRWHF, WHFIFW, IWLSGLSRGVWVSFP, and GSRILTFRSGSWYAS and derivs. based upon these sequences. Comprns. and the use of the peptides in inhibiting cell cycle progression, such as in uncontrolled cell proliferation, are also provided.

IT **286839-16-5P**

RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); SPN (Synthetic preparation); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)

(peptide sequence; transcription factor E2F DNA-binding domain inhibitor peptides and uses thereof)

IT **286839-22-3 286839-23-4**

RL: PRP (Properties)

(unclaimed sequence; transcription factor E2F DNA-binding domain inhibitor peptides and uses thereof)

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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E1 THROUGH E3 ASSIGNED

=> fil reg
FILE 'REGISTRY' ENTERED AT 13:50:51 ON 13 FEB 2003
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STRUCTURE FILE UPDATES: 12 FEB 2003 HIGHEST RN 469395-83-1
DICTIONARY FILE UPDATES: 12 FEB 2003 HIGHEST RN 469395-83-1

TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP PROPERTIES for more information. See STNote 21, Searching Properties in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnote21.pdf

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1 [illegible] E1

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                  L2 OR L3)

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RN   286839-23-4  REGISTRY
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     (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   13: PN: WO0044771 SEQID: 22 unclaimed sequence
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REFERENCE   1:  133:145915

L8   ANSWER 2 OF 3  REGISTRY  COPYRIGHT 2003 ACS
RN   286839-22-3  REGISTRY
CN   L-Phenylalanine, L-tryptophyl-L-alanyl-L-arginyl-L-tryptophyl-L-histidyl-
     (9CI)  (CA INDEX NAME)
OTHER NAMES:
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HITS AT:   1-6

REFERENCE   1:  133:145915

L8   ANSWER 3 OF 3  REGISTRY  COPYRIGHT 2003 ACS
RN   286839-16-5  REGISTRY
CN   L-Phenylalanine, L-tryptophyl-L-valyl-L-arginyl-L-tryptophyl-L-histidyl-
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SQL  6
RN   286839-16-5  REGISTRY

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L11           26 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L6 NOT L7


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L11  ANSWER 1 OF 26  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:          2002:850304  HCAPLUS
DOCUMENT NUMBER:           137:347570
TITLE:                     Cloning and cDNA and deduced amino acid sequences of
                           69 human proteins and their diagnostic and therapeutic
                           uses
INVENTOR(S):               Ruben, Steven M.; Parish, Steven M.; Rosen, Craig A.;
                           Birse, Charles E.
PATENT ASSIGNEE(S):        Human Genome Sciences, Inc., USA
SOURCE:                    U.S. Pat. Appl. Publ., 194 pp., Cont.-in-part of Appl.
                           No. PCT/US01/01346.
                           CODEN: USMXCO
DOCUMENT TYPE:             Patent
LANGUAGE:                  English
FAMILY ACC. NUM. COUNT:    90
PATENT INFORMATION:

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     US 20021651 37      A1   20021107      US 2001-860670   20010521
     WO 2001055449       A1   20010802      WO 2001-US1346   20010117
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
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             SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
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             BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     AU 2001050770       A5   20010807      AU 2001-50770    20010117
     US 20020042096      A1   20020411      US 2001-764847   2001 1117
     US 20020077270      A1   20020620      US 2001-764848   2001 1117
     US 20020086811      A1   20020704      US 2001-764861   2001 1117
     US 20020086820      A1   20020704      US 2001-764862   20010117
     US 20020086821      A1   20020704      US 2001-764881   20010117
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     US 20020086823      A1   20020704      US 2001-764889   20010117
     US 20020086830      A1   20020704      US 2001-764893   20010117
     US 20020086835      A1   20020711      US 2001-764878   20010117
     US 20020086874      A1   20020711      US 2001-764903   20010117
     US 20021 4873       A1   20020718      US 2001-764907   20010117
     US 20021 2684       A1   20020801      US 2001-764840   20010117
     US 20021 8819       A1   20020829      US 2001-764885   20010117
     US 20021 4 7        A1   20020912      US 2001-764847   20010117
     US 20021 4714       A1   20021010      US 2001-764877   2001 117


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US 2002173454	A1	20021121	US 2001-764904	20010117
US 2003013649	A1	20030116	US 2001-989442	20011121

PRIORITY APPLN. INFO.:

US 2000-179065P	P	20000131
US 2000-179065P	P	20000131
US 2000-180628P	P	20000204
US 2000-181628P	P	20000204
US 2000-2[illegible]515P	P	[illegible]
US 2000-216[illegible]P	P	[illegible]
US 2000-216[illegible]P	P	20000714
US 2000-2254[illegible]P	P	[illegible]814
US 2000-229343P	P	20000901
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US 2000-246526P	P	20001108
US 2000-246529P	P	20001108
US 2000-249210P	P	20001117
US 2000-249211P	P	20001117
US 2000-249214P	P	20001117
US 2000-249265P	P	20001117
US 2000-250160P	P	20001201
US 2000-250391P	P	20001201
US 2000-251030P	P	20001205
US 2000-251988P	P	20001205
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US 2000-251479P	P	[illegible]
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US 2001-764859	A2	[illegible]
WO 2001-US1346	A2	[illegible]
US 2000-214886P	P	20000628
US 2000-216647P	P	20000707
US 2000-217487P	P	20000711
US 2000-217496P	P	20000711
US 2000-220963P	P	20000726
US 2000-220964P	P	20000726
US 2000-224518P	P	20000814
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US 2000-236327P	P	20000929	
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US 2000-237040P	P	20001002	
US 2000-241785P	P	20001020	
US 2000-241809P	P	20001020	
US 2000-244617P	P	20001101	
US 2000-249299P	P	20001117	
US 2000-251356P	P	20001208	
US 2000-251868P	P	20001208	
US 2000-251869P	P	20001208	
US 2001-764863	B1	20010117	

AB The present invention relates to 69 novel human proteins and isolated nucleic acids contg. the coding regions of the genes encoding such proteins. Tissue distribution, sequence homologies, and preferred epitope sites are provided for the proteins, as well as chromosomal mapping of some of the genes. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human proteins in bacterial, insect, and mammalian cells. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human proteins. High-throughput screening assays are also provided for various putative activities of the proteins.

IT **474183-38-5P**, Protein (human clone HFIED13)
RL: BPN (Biosynthetic preparation ; BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; cloning and cDNA and deduced amino acid sequences of 69 human proteins and their diagnostic and therapeutic uses)

L11 ANSWER 2 OF 26 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:723049 HCAPLUS
DOCUMENT NUMBER: 137:227411
TITLE: Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
AUTHOR(S): Fleischmann, R. D.; Alland, D.; Eisen, J. A.; Carpenter, L.; White, O.; Peterson, J.; DeBoy, R.; Dodson, R.; Gwinn, M.; Haft, D.; Hickey, E.; Kolonay, J. F.; Nelson, W. C.; Umayam, L. A.; Ermolaeva, M.; Salzberg, S. L.; Delcher, A.; Utterback, T.; Weidman, J.; Khouri, H.; Gill, J.; Mikula, A.; Bishai, W.; Jacobs, W. R., Jr.; Venter, J. C.; Fraser, C. M.
CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA
SOURCE: Journal of Bacteriology [illegible], [illegible], 2[illegible]
CODEN: JOBAAY; ISSN: [illegible]
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Virulence and immunity are poorly understood in Mycobacterium tuberculosis. The complete genome of the M. tuberculosis clin. strain CDC1551 was sequences and a whole-genome comparison with the lab. strain H37Rv performed in order to identify polymorphic sequences with potential relevance to disease pathogenesis, immunity, and evolution. Large-sequence and single-nucleotide polymorphisms were found in numerous genes. Polymorphic loci included a phospholipase C, a membrane lipoprotein, members of an adenylate cyclase gene family, and members of the PE/PPE gene family, some of which have been implicated in virulence or the host immune response. Several gene families, including the PE/PPE gene family, also had significantly higher synonymous and nonsynonymous

substitution frequencies compared to the genome as a whole. A large sample of M. tuberculosis clin. isolates was tested for a subset of the large-sequence and single-nucleotide polymorphisms and widespread genetic variability was found at many of these loci. Phylogenetic and epidemiol. anal. was carried out to investigate the evolutionary relationships among isolates and the origins of specific polymorphic loci. A no. of these polymorphisms appear to have occurred multiple times as independent events, suggesting that these changes may be under selective pressure. Together, these results demonstrate that polymorphisms among M. tuberculosis strains are more extensive than initially anticipated, and genetic variation may have an important role in disease pathogenesis and immunity. The sequence of the clin. strain CDC1551 of M. tuberculosis was deposited in GenBank/EMBL/DDBJ under accession no. AE000516, and the sequence of the genome of the M. tuberculosis lab. strain H37Rv was recently sequenced and deposited as [illegible].

IT 457684-48-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; whole-genome comparison of Mycobacterium tuberculosis clin. and lab. strains)

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 3 OF 26 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:545718 HCAPLUS
DOCUMENT NUMBER: 137:74287
TITLE: The genome of Methanosarcina mazei: evidence for lateral gene transfer between bacteria and Archaea
AUTHOR(S): Deppenmeier, Uwe; Johann, Andre; Hartsch, Thomas; Merkl, Rainer; Schmitz, Ruth A.; Martinez-Arias, Rosa; Henne, Anke; Wiezer, Arnim; Baumer, Sebastian; Jacobi, Carsten; Bruggemann, Holger; Lienard, Tanja; Christmann, Andreas; Bomeke, Mechthild; Steckel, Silke; Bhattacharyya, Anamitra; Lykidis, Athanasios; Overbeek, Ross; Klenk, Hans-Peter; Gunsalus, Robert P.; Fritz, Hans-Joachim; Gottschalk, Gerhard
CORPORATE SOURCE: Gottingen Genomics Laboratory. Department of General Microbiology. Institute of Microbiology and Genetics, Georg-August-University, Goettingen, D-37077, Germany
SOURCE: Journal of Molecular Microbiology and Biotechnology (2002), 4(4), 453-461
CODEN: JMMBFF; ISSN: 1464-1801
PUBLISHER: Horizon Scientific Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The Archaeon Methanosarcina mazei and related species are of great ecol. importance as they are the only organisms fermenting acetate, methylamines and methanol to methane, carbon dioxide and ammonia (in case of methylamines). Since acetate is the precursor of 60% of the methane produced on earth those organisms contribute significantly to the prodn. of this greenhouse gas, e.g. in rice paddies. The 4,096,345 base pairs circular chromosome of M. mazei is more than twice as large as the genomes of the methanogenic Archaea currently completely sequenced. There were 3371 open reading frames (ORFs) identified. Based on currently available sequence data 376 of these ORFs are Methanosarcina-specific and 1043 ORFs find their closest homolog in the bacterial domain. About 544 of these ORFs reach significant similarity values only in the bacterial domain. They include [illegible] examples are the occurrence of the bacterial [illegible] system and the presence of tetrahydrofolate-dependent enzymes. These findings might indicate that lateral gene transfer has played an important

evolutionary role in forming the physiol. of this metabolically versatile methanogen. The genome sequence is deposited in GenBank under Accession No. AE008644.

IT **440301-84-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Methanosarcina mazei and evidence for lateral gene transfer between Archaea and Bacteria)

REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 4 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:348600 HCAPLUS
DOCUMENT NUMBER: 137:[illegible]
TITLE: Human genome derived single exon nucleic acid probes useful for gene expression analysis
INVENTOR(S): Penn, Sharron Gaynor; Rank, David Russell; Chen, Wenshen; Hansel, David Kagen
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 87 pp., Cont.-in-part of U.S. Ser. No. 774,203.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 84
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002048763	A1	20020425	US 2001-864761	20010523
GB 2360284	A1	20010919	GB 2000-24263	20001004
GB 2360284	B2	20020227		
GB 2361238	A1	20011017	GB 2001-15281	20001004
GB 2361238	B2	20020306		
US 2002081590	A1	20020627	US 2001-774203	20010129
WO 2001057271	A2	20010809	WO 2001-US661	20010130
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WO 2001057274      A2    [illegible]          WO [illegible]-[illegible]      [illegible]
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          BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
WO 2001057275      A2    20010809          WO 2001-US667      20010130
WO 2001057275      C2    20021017
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          BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
WO 2001057276      A2    20 10809          WO 2001-US668      20010130
WO 2001057276      A3    20 30109
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WO 2001057277      A2    20 10809          WO 2001-US669      20010130
      W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
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          SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
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WO [illegible]      A2    [illegible]          WO [illegible]-[illegible]      [illegible]
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BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
WO 2001113866003 A2 20011118 WO 2001-US665 20010130
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
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DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
US 20020102252 A1 20020801 US 2001-847995 20010406
PRIORITY APPLN. INFO.: US 2000-193812P P 20000330
US 2000-217458P P 20000711
US 2000-606438 A2 20000630
US 2000-632366 A2 20000803
US 2000-234687P P 20000921
US 2000-236359P P 20000927
GB 2000-24263 A 20001004
US 2001-774203 A2 20010129
WO 2001-US661 A2 20010130
WO 2001-US662 A2 20010130
WO 2001-US663 A2 20010130
WO 2001-US664 A2 20010130
WO 2001-US665 A2 20010130
WO 2001-US666 A2 20010130
WO 2001-US667 A2 20010130
WO 2001-US668 A2 20010130
WO 2001-US669 A2 20010130
WO 2001-US670 A2 20010130
US 2001-160581P P 20010518

AB Methods and app. for predicting, confirming and displaying functional regions from genomic sequence data are used to identify 16,834 unique human genome-derived single exon probes useful for gene expression anal., particularly gene expression anal. by microarray. Also presented are genome-derived single exon microarrays that include such probes, peptides encoded by the exons, and antibodies thereto. The human genome-derived single-exon probes are known to be expressed in one or more human tissues or cell types, particularly human brain, heart, liver, fetal liver,placenta, lung, bone marrow, BT474 and other human mammary epithelial cells, HeLa and other human cervical epithelial cells, and HBL 100 and other human mammary epithelial cells. The invention provides a method of financing, selling and/or licensing genome-derived single-exon microarrays to customer desiring to measure gene expression, comprising: making available for computerized query or subscription service a database having a record corresponding to each genome-derived single exon microarray available for sale and or license. [This abstr. record is one of ten records for this document terminated by the [illegible] index entries required to fully index the [illegible] constraints.].

IT **437115-91-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; human genome derived single exon nucleic acid probes useful for gene expression anal.)

L11 ANSWER 6 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: [illegible] HCAPLUS
DOCUMENT NUMBER: [illegible]
TITLE: Complete genome sequence of Methanosarcina acetivorans C2A reveals extensive metabolic and physiological diversity

AUTHOR(S): [illegible]; Galagan, James E.; Nusbaum, Chad; Lyons, Nicholas; Endrizzi, Matthew G.; Maruyama, Hisakazu; Kozhukhar, Fitz-Hugh, Will; Calvo, Sarah; Engels, Reinhard; Smirnov, Serge; Atnoor, Daren; Brown, Adam; Allen, Nicole; Naylor, Jerome; Stange-Thomann, Nicole; DeArellano, Kurt; Johnson, Robin; Linton, Lauren; McEwan, Paul; McKernan, Kevin; Talamas, Jessica; Tirrell, Andrea; Ye, Wenjuan; Zimmer, Andrew; Barber, Robert D.; Cann, Isaac; Graham, David E.; Grahame, David A.; Guss, Adam M.; Hedderich, Reiner; Ingram-Smith, Cheryl; Kuettner, H. Craig; Krzycki, Joseph A.; Leigh, John A.; Li, Weixi; Liu, Jinfeng; Mukhopadhyay, Biswarup; Reeve, John N.; Smith, Kerry; Springer, Timothy A.; Umayam, Lowell A.; White, Owen; White, Robert H.; de Macario, Everly Conway; Ferry, James G.; Jarrell, Ken F.; Jing, Hua; Macario, Alberto J. L.; Paulsen, Ian; Pritchett, Matthew; Sowers, Kevin R.; Swanson, Russell V.; Zinder, Steven H.; Lander, Eric; Metcalf, William W.; Birren, Bruce

CORPORATE SOURCE: Whitehead Institute/Center for Genome Research, Cambridge, MA, 02141, USA

SOURCE: Genome Research (2002), 12(4), 532-542
CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Methanogenesis, the biol. prodn. of methane, plays a pivotal role in the global carbon cycle and contributes significantly to global warming. The majority of methane in nature is derived from acetate. The complete genome sequence of an acetate-utilizing methanogen, Methanosarcina acetivorans C2A, is now reported. Methanosarcineae are the most metabolically diverse methanogens, thrive in a broad range of environments, and are unique among the Archaea in forming complex multicellular structures. This diversity is reflected in the genome of M. acetivorans. At 5,751,492 base pairs it is by far the largest known archaeal genome. The 4524 open reading frames code for a surprisingly wide and unanticipated variety of metabolic and cellular capabilities. The presence of novel methyltransferases indicates the likelihood of undiscovered natural energy sources for methanogenesis, whereas the presence of single-subunit carbon monoxide dehydrogenases raises the possibility of nonmethanogenic growth. Although motility has not been obsd. in any Methanosarcineae, a flagellin gene cluster and two complete chemotaxis gene clusters were identified. The availability of genetic methods, coupled with its physiol. and metabolic diversity, makes M. acetivorans a powerful model organism for the study of archaeal biol. The genome sequence is deposited in GenBank under Accession No. AE010656-AE011189.

IT **406874-66-6**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Methanosarcina acetivorans C2A reveals extensive metabolic and physiol. diversity)

REFERENCE COUNT: 78 THERE ARE 78 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 6 OF 26 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:[illegible] HCAPLUS

DOCUMENT NUMBER: 137:[illegible]

TITLE: Functional annotation of a full-length Arabidopsis cDNA collection

AUTHOR(S): [illegible]; Kikuchi, Shoshi; Satoh, Kenji; Nagata, Aiko; Kawagashira, Naoko; Doi, Kazuyuki; Mishima, Keiko; Yamamoto, Kimiko; Yamada, Kenji; Daosukho, Chanin; Slunt, Jonathan; Hudson, Jennifer; Beckstrom-Sternberg, Stephen; Altaf-Ul-Amin, Md.; Asai, Kiyoshi; Shibata, Daisuke; Nishikawa, Tadashi; Hayashizaki, Yoshihide; Kay, Alan; Myers, Gene; Nakai, Kenta; Kikuchi, Shoshi;

Muramatsu, Masami; Hayashizaki, Yoshihide; Kawai, Jun; Carninci, Piero; Itoh, Masayoshi; Ishii, Yoshiyuki; Arakawa, Takahiro; Shibata, Kazuhiko; Shinagawa, Akira; Shibata, Kazuo

CORPORATE SOURCE: Plant Molecular Expression Team, Plant Functional Genomics Res. Group, RIKEN Genomic Sciences Center (GSC), 1-1-1 Koyadai, Tsukuba, 305-0074, Japan

SOURCE: Science (Washington, DC, United States), 296(5565), 141-145
CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Full-length cDNAs are essential for the correct annotation of genomic sequences and for the functional anal. of genes and their products. About 155,144 RIKEN Arabidopsis full-length (RAFL) cDNA clones were isolated. The 3'-end expressed sequence tags (ESTs) of 155,144 RAFL cDNAs were clustered into 14,668 nonredundant cDNA groups, about 60% of predicted genes. 5'-ESTs were also obtained from 14,034 nonredundant cDNA groups and a promoter database constructed. The sequence database of the RAFL cDNAs is useful for promoter anal. and correct annotation of predicted transcription units and gene products. Furthermore, the full-length cDNAs are useful resources for analyses of the expression profiles, functions, and structures of plant proteins. [This abstr. record is one of sixteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **437141-30-5**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; human gene encoding a full-length Arabidopsis cDNA collection)

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 7 OF 26 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:173787 HCAPLUS

DOCUMENT NUMBER: 136:351357

TITLE: Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human adult liver

INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng; Rank, David R.

PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA

SOURCE: PCT Int. Appl., 659 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 84

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002018573	A2	20020307	WO 2001-US27564	20010831
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
US 2002164634	A1	20021107	US 2001-944263	20010831

AU [illegible]	A1	[illegible]			
GB 2361241	A1	20011017	GB 2001-15291	20010604	
GB 2361241	B2	20020306			
WO [illegible]	A2	20010802	WO 2001-US664	20010130	

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RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US [illegible]	A1	[illegible]	[illegible]	[illegible]

PRIORITY APPLN. INFO.:

[illegible]	[illegible]	[illegible]
US [illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]
US 2000-234687P	P	20000921
US 2000-236359P	P	20000927
GB 2000-24263	A	20001004
WO 2001-US664	A	20010130

AB A single exon nucleic acid microarray comprising 13,109 single exon nucleic acid probes for measuring gene expression in a sample derived from human adult liver is described. These unique exons are within longer probe sequences; sequencing confirms the exact chem. structure of each probe. Some amplicons have more than one exon, and some exons are contained in more than one amplicon. Expression, homol., and functional information are provided for the genome-derived single exon probes that are expressed significantly in human adult liver cells. Also described are 12,886 single exon nucleic acid probes and 12,583 proteins expressed in the adult liver and their use in methods for detecting gene expression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression data. Methods are provided for identifying exons in a genomic DNA sequence, and for assigning exons to a single gene.

IT **420924-39-6**

RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human adult liver)

L11 ANSWER 6 OF 26 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER:	2002:157787 HCAPLUS
DOCUMENT NUMBER:	136:195341
TITLE:	Cloning and cDNA and deduced amino acid sequences of 21 human secreted proteins
INVENTOR(S):	Rosen, Craig A.; Komatsoulis, George A.; Baker, Kevin P.; Birse, Charles E.; Soppet, Daniel R.; Olsen, Henrik S.; Moore, Paul A.; Wei, Ping; Ebner, S.; Ruben, S. [illegible]; Li, Y. [illegible]; [illegible], Y. H.; Ni, J.; Reynolds, Michele; Ni, Jian
PATENT ASSIGNEE(S):	Human Genome Sciences, Inc., USA
SOURCE:	PCT Int. Appl., 184 pp. CODEN: PIXXD2
DOCUMENT TYPE:	Patent
LANGUAGE:	English
FAMILY ACC. NUM. COUNT:	1
PATENT INFORMATION:	

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 02/12473 A1 20020214 W [illegible]
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 2001084424 A 20020218
AU 2001-84424 20010807
PRIORITY APPLN. INFO.: US 2000-224242P P 20000807
US 2001-812414 A 20010319
WO 2001-US24435 W 20010807

AB The present invention relates to 21 novel human secreted proteins and isolated nucleic acids cont. the coding regions of the genes encoding such proteins. Tissue distribution, sequence homologies, and preferred epitope sites are provided for the secreted proteins, as well as chromosomal mapping of some of the genes. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins in bacterial, insect, and mammalian cells. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins. High-throughput screening assays are also provided for various putative activities of the secreted proteins.

IT **400696-91-5P**
RL: BSN (Biosynthetic preparation); BST (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; cloning and DNA and deduced amino acid sequences of 21 human secreted proteins)

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 9 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:125123 HCAPLUS
DOCUMENT NUMBER: 136:143954
TITLE: Genome sequence of the plant pathogen Ralstonia solanacearum
AUTHOR(S): Salanoubat, M.; Genin, S.; Artiguenave, F.; Gouzy, J.; Mangenot, S.; Arlat, M.; Billault, A.; Brottier, P.; Camus, J. C.; Cattolico, L.; Chandler, M.; Choisne, N.; Claudel-Renard, C.; Cunnac, S.; Demange, N.; Gaspin, C.; Lavie, M.; Moisan, A.; Robert, C.; Saurin, W.; Schiex, T.; Siguier, P.; Thebault, P.; Whalen, M.; Wincker, P.; Levy, M.; Weissenbach, J.; [illegible], C. A.
CORPORATE SOURCE: [illegible]
SOURCE: Nature (London, United Kingdom) (2002), 415(6871), 497-502
CODEN: NATURS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Ralstonia solanacearum is a devastating, soil-borne plant pathogen with a global distribution and an unusually wide host range. It is a model system for the study of host-microbe interactions. To understand its pathogenicity, the complete genome sequence and its anal. of strain GMI1000 is presented. The 5.8-megabase (Mb) genome is organized into two replicons: a 3.7-Mb chromosome and a 2.1-Mb megaplasmid. Both replicons have a mosaic structure providing evidence for the acquisition of genes through horizontal gene transfer. Regions cont. genetically mobile elements assocd. with the peculiar G+C bias may have an important function in genome evolution. The genome encodes many putative [illegible] with a role in pathogenicity. [illegible]

factors were identified. The complete repertoire of type III secreted effector proteins can be studied. Over 40 candidates were identified. Comparison with other genomes suggests that bacterial plant pathogens and animal pathogens harbor distinct arrays of specialized type III-dependent effectors.

IT 394342-70-2 394342-96-2
BL: BSU (Biological study, unclassified ; PRP (Properties'; BIOL (Biological study)
(amino acid sequence; genome sequence of the plant pathogen Ralstonia solanacearum)

REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 1 OF [illegible] HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: [illegible]
DOCUMENT NUMBER: [illegible]
TITLE: Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta
INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng; Rank, David R.
PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
SOURCE: PCT Int. Appl., 654 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 84
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001057272	A2	20010809	WO 2001-US663	20010130
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
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GB 2360284	A1	20010919	GB 2000-24263	20001004
GB 2360284	B2	20020227		
GB 2361238	A1	20011017	GB 2001-15281	20001004
GB 2361238	B2	20020306		
WO 2001057272	A2	20010809	WO 2001-US663	20010130
WO 2001057272	A3	20020103		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US [illegible]	A1	[illegible]	[illegible]	[illegible]

PRIORITY APPLN. INFO.: [illegible]

PB ... -24167 A ... 1 ...
WO ...-US663 A 20010130

AB A single exon nucleic acid microarray comprising 13,111 single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta is described. Three multiple exon gene microarray probe sequences; sequencing primers for exon ... with gaps. Some splicing variants of the genes, and open reading frames contained in more than one amplicon, expression, tissue, and chromosomal information are provided for the genome-derived single exon probes that are expressed significantly in human placenta. Also described are 13,111 single exon nucleic acid probes and 12,605 proteins expressed in the placenta cells and their use in methods for detecting gene expression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exons to a single gene. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **400664-75-7**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human placenta)

L11 ANSWER 11 OF 14 HCAPLUS COPYRIGHT ... ACS
ACCESSION NUMBER: 2002:11[illegible] HCAPLUS
DOCUMENT NUMBER: 136:195268
TITLE: Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver
INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng; Rank, David R.
PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
SOURCE: PCT Int. Appl., 639 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 54
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001[illegible]	A2	2001[illegible]	[illegible]	[illegible]
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
GB 2360284	A1	20010919	GB 2000-24263	20001004
GB 2360284	B2	2002[illegible]		
GB 2361236	A1	20011017	GB 2001-15281	20001004
GB 2361236	B2	2002[illegible]		
WO 2001[illegible]	A1	20010419	WO 2001-US663	20010130
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2002142454 A1 20021003 US 2001-827395 20010406

PRIORITY APPLN. INFO.: US 2000-195312P P 20000407
US 2000-207456P P 20000526
US 2000-608408 A 20000630
US 2000-632306 A 20000803
US 2000-234687P P 20001021
US 2000-240372P P 20001017
US 2001-814,114 A 20010406

AB A single exon nucleic acid microarray comprising 1,[illegible] single exon nucleic acid probes for measuring gene expression in a sample derived from human fetal liver cells is described. These unique exons are within longer probe sequences; regardless of the exact chem. structure of each probe. Some amplicons have more than one exon, and some exons are contained in more than one amplicon. Expression, homol., and functional information are provided for the non-redundant single exon probes that are expressed significantly in human fetal liver cells. Also described are 12,456 single exon nucleic acid probes and 12,027 proteins expressed in the fetal liver and their use in methods for detecting gene expression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exons to a single gene. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 400957-73-5
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human fetal liver)

L11 ANSWER 12 OF 26 HCAPLUS COPYRIGHT 2004 ACS
ACCESSION NUMBER: [illegible] HCAPLUS
DOCUMENT NUMBER: [illegible]
TITLE: Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain
INVENTOR(S): Penn, Sharron G.; Hansel, David K.; Chen, Wensheng; Rank, David R.
PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
SOURCE: PCT Int. Appl., 650 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 64
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001087276	A2	20011122	WO 2001-US[illegible]	20010[illegible]

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA [illegible] A1 [illegible] CA [illegible]
AU [illegible] A5 [illegible]

GB 2361238 A1 [illegible] GB 2[illegible]
GB [illegible] B2 [illegible]
WO 2001057278 A2 [illegible] WO 2[illegible]
W [illegible]

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
US [illegible] A1 [illegible] US 2[illegible]
PRIORITY APPLN. INFO.: US 2000-606408 A 20000630
US 2000-632366 A 20000803

AB A single exon nucleic acid microarray comprising 12,821 single exon nucleic acid probes for measuring gene expression in a sample derived from human brain cells is described. These unique exons are within longer probe sequences; sequencing confirms the exact chem. structure of each probe. Some amplicons have more than one exon, and some exons are contained in more than one amplicon. Expression, homol., and functional information are provided for the genome-derived single exon probes that are expressed significantly in human brain. Also described are 12,613 single exon nucleic acid probes and 12,377 proteins expressed in the brain and their use in methods for detecting gene expression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exons to a single gene. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **412969-90-5**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human brain)

L11 ANSWER 10 OF 24 HCAPLUS COPYRIGHT [illegible] ACS
ACCESSION NUMBER: [illegible]
DOCUMENT NUMBER: [illegible]
TITLE: [illegible] useful for analysis of gene expression in human bone marrow
INVENTOR(S): Penn, Sharron G.; Hamzeh, David K.; Chen, Wensheng; Rank, David R.
PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
SOURCE: PCT Int. Appl., [illegible] pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 64
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO [illegible]	A1	[illegible]	WO [illegible]	[illegible]

W: AB, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

GB 2361284 A1 20011017 GB 2000-24263 20001004
GB 2360284 B2 20020227
GB 2361239 A1 20011017 GB 2001-10081 20010404
GB 2361239 B2 20020515
WO 2001075707A2 A1 20011011 WO 2001-US8669 20010316
WO 2001075707A3 A2 20020418

W: AB, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 20020119466 A1 20020829 US 2001-817998 20010326
PRIORITY APPLN. INFO.: US 2000-180312P P 20000204
US 2000-207456P P 20000526
US 2000-608408 A 20000630
US 2000-632366 A 20000803
US 2000-234687P P 20000921
US 2000-236359P P 20000927
GB 2000-24263 A 20001004
WO 2001-US8669 A 20010316

AB A single exon nucleic acid microarray comprising [illegible] single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow is described. These unique exons are within longer probe sequences; sequencing confirms the exact chem. structure of each probe. Some amplicons have more than one exon, and some exons are contained in more than one amplicon. Expression, homol., and functional information are provided for the genome-derived single exon probes that are expressed significantly in human bone marrow. Also described are 12,898 single exon nucleic acid probes and 12,616 proteins expressed in the bone marrow and their use in methods for detecting gene expression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exons to a single gene. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **402671-83-4**
RL: ANT (Analyte); BAC (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human bone marrow)

L11 ANSWER 14 OF 16 [illegible] COPYRIGHT [illegible] ACS
ACCESSION NUMBER: [illegible]
DOCUMENT NUMBER: [illegible]
TITLE: Human nucleic acids and their encoded proteins and methods
INVENTOR(S): Roser, Inna A.; Barash, Steven C.; Burns, Steven M.

PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA
SOURCE: PCT Int. Appl., [illegible] pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: [illegible]
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001[illegible]	A1	[illegible]	WO 2001-[illegible]	[illegible]

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
AU 2001041413	A5	[illegible]	AU 2001-41413	20010117
AU 2001041416	A5	20010807	AU 2001-41416	20010117
AU 2001041417	A5	20010807	AU 2001-41417	20010117
AU 2001050770	A5	20010807	AU 2001-50770	20010117
US 2002042096	A1	20020411	US 2001-[illegible]	20010117
US 2002077270	A1	20020620	US 2001-[illegible]	[illegible]
US 2002086811	A1	20020704	US 2001-[illegible]	[illegible]
US [illegible]	A1	[illegible]	[illegible]	[illegible]
US 2002086821	A1	20020704	US 2001-[illegible]	[illegible]
US 2002086822	A1	20020704	US 2001-764886	20010117
US 2002086823	A1	20020704	US 2001-764889	20010117
US 2002086330	A1	20020704	US 2001-764893	20010117
US 2002090615	A1	20020711	US 2001-764878	20010117
US 2002090674	A1	20020711	US 2001-764903	20010117
US 2002094953	A1	20020718	US 2001-764860	20010117
US 2002102638	A1	20020801	US 2001-764846	20010117
US 2002119919	A1	20020829	US 2001-764855	20010117
US 2002132767	A1	20020919	US 2001-764847	20010117
US 2002147140	A1	20021010	US 2001-764877	20010117
US 2002151479	A1	20021017	US 2001-764873	20010117
US 2002161208	A1	20021031	US 2001-764884	20010117
US 2002164685	A1	20021107	US 2001-764857	20010117
US 2002173454	A1	20021121	US 2001-764904	20010117
EP 1261703	A1	20021204	EP 2001-[illegible]	[illegible]

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
AU 2001052879	A5	[illegible]	AU [illegible]	[illegible]
AU 2001043137	A5	20010814	AU 2001-43137	[illegible]
US 2003013649	A1	[illegible]	US 2001-[illegible]	[illegible]

PRIORITY APPLN. INFO.:

US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]

US 2000-249263P	P	20001117
US 2000-249264P	P	20001117
US 2000-249265P	P	20001117
US 2000-249297P	P	20001117
US 2000-249299P	P	20001117
US 2000-249317P	P	20001117
[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]
US 2000-251924P	P	20001206
US 2000-256719P	P	20001205
US 2000-251479P	P	20001206
US 2000-251856P	P	20001208
US 2000-251868P	P	20001208
US 2000-251869P	P	20001208
US 2000-251990P	P	20001208
US 2001-764863	B1	20010117
WO 2001-US1338	W	20010117

AB The present invention relates to novel musculoskeletal system-related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "musculoskeletal system antigens", and the use of such musculoskeletal system antigens for detecting disorders of the musculoskeletal system, particularly the presence of cancer and cancer metastases. More specifically, 1023 isolated musculoskeletal system-assocd. cDNA mols. are provided encoding novel musculoskeletal system-assocd. polypeptides. Novel musculoskeletal system polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human musculoskeletal system assocd. polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the musculoskeletal system, including cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compns. for inhibiting the prodn. and function of the polypeptides of the present invention.

IT **384873-95-4P**

RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(amino acid sequence; human musculoskeletal system-specific nucleic acids and their encoded proteins and antibodies)

L11 ANSWER 15 OF 26 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:763025 HCAPLUS

DOCUMENT NUMBER: 135:338111

TITLE: Albumin fusion proteins with therapeutic proteins for improved shelf-life

INVENTOR(S): Rosen, Craig A.; Haseltine, William A.

PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA

SOURCE: PCT Int. Appl., [illegible] pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001070137	A1	20011018	WO 2001-US11988	20010412

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,

HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,
LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,
RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ,
VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
EP 1[illegible] A1 [illegible] EP 2001-944114 [illegible]
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
PRIORITY APPLN. INFO.: US 2000-228[illegible]P P [illegible]
US 2000-18[illegible]P P [illegible]
US 2000-25[illegible]P P [illegible]
WO 2001-US11[illegible] W [illegible]

AB The present invention encompasses fusion proteins of albumin with various therapeutic proteins. Therapeutic proteins may be stabilized to extend the shelf-life, and/or to retain the therapeutic protein's activity for extended periods of time in soln., in vitro and/or in vivo, by genetically or chem. fusing or conjugating the therapeutic protein to all or a fragment or variant of albumin. The fusion proteins may also reduce the need to formulate the protein soln. with large excesses of carrier proteins to prevent loss of therapeutic proteins due to factors such as binding to the container. Nucleic acid mols. encoding the albumin fusion proteins of the invention are also encompassed by the invention, as are vectors contg. these nucleic acids, host cells transformed with these nucleic acids vectors, and methods of making the albumin fusion proteins of the invention and using these nucleic acids, vectors, and/or host cells. Thus, plasmid vectors are constructed in which DNA encoding the desired therapeutic protein may be inserted for expression of the albumin fusion proteins in yeast (pPPC0005) and mammalian cells (pC4:HSA). Yeast-derived signal sequences from Saccharomyces cerevisiae invertase SUC2 gene, or the stanniocalcin or native human serum albumin signal peptides, are used for secretion in yeast or mammalian systems, resp. Thus, the fusion product of human growth hormone with residues 1-387 of human serum albumin retains essentially intact biol. activity after 6 wk of incubation in tissue culture media at 37.d-[illegible]., whereas recombinant human growth hormone used as control lost [illegible]% activity in the first week. Although the potency of the albumin fusion proteins is slightly lower than the unfused counterparts in rapid in vitro assays, their biol. stability results in much higher biol. activity in the longer term in vitro assay or in vivo assays. Addnl., the present invention encompasses pharmaceutical compns. comprising albumin fusion proteins and methods of treating, preventing, or ameliorating diseases, disorders or conditions using albumin fusion proteins of the invention.

IT 369644-05-3
RL: PRP (Properties)
(unclaimed protein sequence; albumin fusion proteins with therapeutic proteins for improved shelf-life)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 16 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:[illegible] HCAPLUS
DOCUMENT NUMBER: 135:[illegible]
TITLE: Nucleic acids and their encoded polypeptides from human bone marrow
INVENTOR(S): Ford, John E.; Boyle, Bryan J.; Tang, Y. Tom; Liu, Chenghua; Asundi, Vinod; Chen, Ping; Wu, Alfred J.; Ren, Feiyan; Drmanac, Radoje T.
PATENT ASSIGNEE(S): Hyseq, Inc., USA
SOURCE: PCT Int. Appl., [illegible] pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001-34847	A2	20010518	WO 2000-US31782	20001116

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 2001034847 A5 20010514 AU 2001-34847 20010205

PRIORITY APPLN. INFO.:			
US 2000-496914	A	20000203	
US 2000-598075	A	20000620	
US 2000-620325	A	20000719	
US 2000-2505838P	A	20001130	
WO 2001-US3782	W	20010205	

AB The present invention provides a collection or library of 94 nucleic acid contig sequences assembled from expressed sequence tag or cDNA libraries isolated mainly by sequencing by hybridization (SBH), std. PCR, Sanger sequencing techniques, and in some cases, sequences obtained form one or more public databases. The cDNA libraries are from human bone marrow sources and nearest neighbor sequence homol. data are provided. The invention also relates to the proteins encoded by said nucleic acids, along with therapeutic, diagnostic and research utilities for the polynucleotides and proteins.

IT **353568-97-5 354113-34-1**
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; nucleic acids and their encoded polypeptides from human bone marrow)

L11 ANSWER 17 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:566854 HCAPLUS
DOCUMENT NUMBER: 135:163414
TITLE: Human nucleic acids and their encoded proteins and antibodies
INVENTOR(S): Rosen, Craig A.; Barash, Steven C.; Ruben, Steven M.
PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA
SOURCE: PCT Int. Appl., 832 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001056614	A2	20010809	WO 2001-US3782	20010205

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU [illegible] A1 [illegible] AU [illegible] 2001011[illegible]
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US [illegible] A1 [illegible] US [illegible]-764[illegible] [illegible]
US [illegible] A1 [illegible] US [illegible]-764[illegible] [illegible]
US 2002[illegible] A1 2002[illegible] US 2001-764[illegible] 2001011[illegible]
US 2002[illegible] A1 20020704 US 2001-764881 20010117
US 2002[illegible] A1 20020704 US 2001-764886 20010117
US 2002[illegible] A1 20020704 US 2001-764889 20010117
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US 2002090674 A1 20020711 US 2001-764903 20010117
US 2002094[illegible] A1 [illegible] US [illegible] [illegible]
US 2002[illegible] A1 [illegible] US [illegible] [illegible]
US 2002119[illegible] A1 [illegible] US [illegible] [illegible]
US 2002132[illegible] A1 2002091[illegible] US [illegible] [illegible]
US 2002147140 A1 2002101[illegible] US 2001-7648[illegible] 20010117
US 2002151479 A1 2002101[illegible] US 2001-764873 20010117
US 2002161[illegible] A1 [illegible] US 2001-7648[illegible] 20010117
US 2002164686 A1 2002111[illegible] US 2001-764887 20010117
EP 1255869 A1 20021113 EP 2001-916067 20010117
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
US 2002173454 A1 20021121 US 2001-764904 20010117
US 2002165137 A1 20021107 US 2001-860670 20010521
US 2003013649 A1 20030116 US 2001-989442 20011121

PRIORITY APPLN. INFO.:
US 2000-179065P P 20000131
US 2000-180628P P 20000204
US 2000-205515P P 20000519
US 2000-216880P P 20000707
US 2000-218290P P 20000714
US 2000-225447P P 20000814
US 2000-229343P P 20000901
US 2000-230437P P 20000906
US 2000-231243P P 20000908
US 2000-234997P P 2000092[illegible]
US [illegible]-236367P P [illegible]
US [illegible] P [illegible]
US [illegible]-2444[illegible]P P [illegible]
US [illegible]-2447[illegible]P P [illegible]
US 2000-246525P P 20001108
US 2000-246526P P 20001108
US 2000-246528P P 20001108
US 2000-249210P P 20001117
US 2000-249211P P 20001117
US 2000-249214P P 20001117
US 2000-249265P P 20001117
US 2000-250160P P 20001201
US 2000-250391P P 20001201
US 2000-251030P P 20001205
US 2000-251988P P 20001205
US 2000-256719P P 20001205
US 2000-251479P P 20001206
US 2000-25[illegible]P P 2000120[illegible]
US [illegible] P [illegible]
US [illegible] P [illegible]
US [illegible] P [illegible]
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US [illegible] P [illegible]

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US [illegible]
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US [illegible]
US 2000-225266P P 20000814
US 2000-225270P P 20000814
US 2000-225757P P 20000814
US 2000-225758P P 20000814
US 2000-226868P P 20000822
US 2000-228924P P 20000830
US 2000-229287P P 20000901
US 2000-229344P P 20000901
US 2000-229345P P 20000901
US 2000-229509P P 20000905
US 2000-229513P P 20000905
US 2000-231413P P 20000908
US 2000-234223P P 20000921
US 2000-234274P P 20000921
US 2000-235834P P 20000927
US 2000-236327P P [illegible]
US [illegible]
US 2000-236369P P [illegible]
US 2000-236370P P 20000929
US 2000-236802P P 20001002
US 2000-237037P P 20001002
US 2000-237039P P 20001002
US 2000-237040P P 20001002
US 2000-241785P P 20001020
US 2000-241808P P 20001020
US 2000-244617P P 20001101
US 2000-249299P P 20001117
US 2000-251856P P 20001208
US 2000-251868P P 20001208
US 2000-251869P P 20001208
US 2001-764859 A2 20010117
US 2001-764863 B1 20010117
WO 2001-US1346 W 20010117

AB The present invention relates to novel human polynucleotides and the polypeptides encoded by these polynucleotides, and the use of such polypeptides for detecting disorders. More specifically, 79 isolated human cDNA mols. are provided encoding novel polypeptides. Antibodies that bind to these polypeptides are also provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing the novel human polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or comps. for inhibiting the prodn. and function of the polypeptides of the present invention.

IT **353554-69-5**, Protein (human clone HFIEC13)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(protein sequences; human nucleic acids and their encoded proteins and antibodies)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 19 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:397059 HCAPLUS
DOCUMENT NUMBER: 135:19431
TITLE: Genes of Physcomitrella patens [illegible]

enzymes of the synthesis of polyunsaturated fatty acids and lipids

INVENTOR(S): Lerchl, Jens; Renz, Andreas; Ehrhardt, Thomas; Reinal, Andreas; Cirpus, Petra; Bischoff, Friedrich; Frank, Markus; Frommi, Annette; Duwenig, Ellen; Schmidt, Ralf-Michael; Fuchs, Ralf

PATENT ASSIGNEE(S): Basf Plant Science Gmbh, Germany

SOURCE: PCT Int. Appl., 116 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001036641	A1	20010525	WO 1999-EP9108	19991125
W: AU, BR, CA, JP, MX, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
WO 2001036494	A2	20010525	WO 2000-EP11615	20001122
WO 2001036494	A3	20011101		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2001019640	A5	20010604	AU 2001-19640	20001122
BR 2000015905	A	20020806	BR 2000-15905	20001122
EP 1282713	A2	20030212	EP 2000-979617	20001122
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				

PRIORITY APPLN. INFO.: WO 1999-EP9108 W 19991125
WO 2000-EP11615 W 20001122

AB Isolated nucleic acid mols., designated LMRP nucleic acid mols., which encode novel LMRPs from e.g. Physcomitrella patens are described. The invention also provides antisense nucleic acid mols., recombinant expression vectors contg. LMRP nucleic acid mols., and host cells into which the expression vectors have been introduced. The invention sill further provides isolated LMRPs, mutated LMRPs, fusion proteins, antigenic peptides and methods for the improvement of the prodn. of a desired compd. from transformed cells, organisms or plants based on genetic engineering of LMRP genes in these organisms.

IT 343286-49-7
RL: BTU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; genes of Physcomitrella patens encoding homologs of enzymes of synthesis of polyunsatd. fatty acids and lipids)

REFERENCE COUNT: [illegible] THERE ARE [illegible] CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER [illegible] OF [illegible] HCAPLUS [illegible]

ACCESSION NUMBER: [illegible]

DOCUMENT NUMBER: [illegible]

TITLE: Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis

INVENTOR(S): Alexandrov, Nikolai; Brover, Vyacheslav; Chen, Nianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.

PATENT ASSIGNEE(S):
SOURCE:
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. OF COUNT: 17
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1034408	A2	20000906	EP 2000-301439	20000225
F: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2300692	AA	20000825	CA 2000-2300692	20000225
CA 2302928	AA	20001006	CA 2000-2302928	20000406
EP [illegible]	A2	20001129	EP [illegible]	20000804
F: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1054060	A2	20001122	EP 2000-304161	20000517
F: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.:

US	1999-[illegible]P	P	19990[illegible]
US	1999-[illegible]P	P	19990[illegible]
US	1999-[illegible]P	P	19990[illegible]
US	1999-[illegible]P	P	19990[illegible]
US	1999-[illegible]P	P	19990[illegible]
US	1999-1463899P	P	19990602
US	1999-1470038P	P	19990803
US	1999-1472047P	P	19990804
US	1999-1473027P	P	19990804
US	1999-1471927P	P	19990805
US	1999-1472607P	P	19990805
US	1999-1473037P	P	19990806
US	1999-1474167P	P	19990806
US	1999-1474937P	P	19990809
US	1999-1479387P	P	19990809
US	1999-1481717P	P	19990810
US	1999-1483197P	P	19990811
US	1999-1483417P	P	19990812
US	1999-1485487P	P	19990813
US	1999-1487417P	P	19990813
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	1999-1287358P	P	19990329
US	1999-1274028P	P	19990401
US	1999-1282348P	P	19990406
US	1999-1287148P	P	19990408
US	1999-1298458P	P	19990416
US	[illegible]	P	[illegible]
US	1999-1304498P	P	19990421
US	1999-1305108P	P	19990423
US	1999-1305918P	P	19990423
US	1999-1314498P	P	19990428
US	1999-1320468P	P	19990430
US	1999-1320478P	P	19990430
US	1999-1320648P	P	19990504
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	1999-1461118P	P	19990511

US 1999-134218P P 19990514
US 1999-134219P P 19990514
US 1999-134221P P 19990514
US 1999-134370P P 19990514
US 1999-134768P P 19990518
US 1999-134941P P 19990518
US 1999-[illegible]P P [illegible]
US [illegible] P [illegible]
US 1999-[illegible]P P [illegible]
US 1999-[illegible]P P [illegible]
US 1999-[illegible]P P [illegible]
US 1999-[illegible]P P [illegible]
US 1999-137222P P 19990601
US 1999-137528P P 19990603
US 1999-137802P P 19990604
US 1999-137784P P 19990607
US 1999-138094P P 19990608

AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA mols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence or as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present expt., but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CA133:162185280 necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **302645-65-4 302645-66-5**
BL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; sequence-detd. DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)

L11 ANSWER 20 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:754707 HCAPLUS
DOCUMENT NUMBER: 133:318296
TITLE: Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis
INVENTOR(S): Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.
PATENT ASSIGNEE(S): Ceres Inc., USA
SOURCE: Eur. Pat. Appl., 339 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 16
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1033405	A2	20000906	EP 2000-301439	20000225
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2300692	AA	20000825	CA 2000-2300692	20000225
CA 2302826	AA	20000906	CA 2000-2302826	20000406
EP 1063294	A2	20001229	EP 2000-303770	20000504

DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE

EP 1104160 A2 20010530 EP 2000-310161 20001117

DE, DK, ES, FI, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE

[illegible]

US	1999-[illegible]P	P	19990[illegible]
US	1999-[illegible]P	P	19990[illegible]
US	1999-[illegible]P	P	19990[illegible]
US	1999-146356P	P	19990802
US	1999-146356P	P	19990802
US	1999-146369P	P	19990802
US	1999-147038P	P	19990803
US	1999-147204P	P	19990804
US	1999-147[illegible]P	P	1999080[illegible]
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US	[illegible]-[illegible]P	P	[illegible]
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US	1999-147416P	P	19990806
US	1999-147493P	P	19990809
US	1999-147[illegible]P	P	1999080[illegible]
US	1999-148171P	P	19990811
US	1999-148319P	P	19990811
US	1999-148341P	P	19990812
US	1999-148565P	P	19990813
US	1999-148654P	P	19990813
US	1999-123180P	P	19990305
US	1999-123548P	P	19990309
US	1999-125788P	P	19990323
US	1999-126264P	P	19990325
US	1999-126785P	P	19990329
US	1999-127462P	P	19990401
US	1999-128334P	P	19990406
US	1999-128[illegible]4P	P	1999040[illegible]
US	1999-128445P	P	19990416
US	1999-130077P	P	19990419
US	1999-130449P	P	19990421
US	1999-130510P	P	19990423
US	1999-130[illegible]1P	P	1999[illegible]23
US	1999-131[illegible]4P	P	1999[illegible]4[illegible]
US	1999-13[illegible]4PP	P	1999[illegible]4[illegible]
US	1999-132[illegible]P	P	19990430
US	1999-132494P	P	19990504
US	1999-132495P	P	19990505
US	1999-132496P	P	19990506
US	1999-132497P	P	19990506
US	1999-132863P	P	19990507
US	1999-134256P	P	19990511
US	1999-134218P	P	19990514
US	1999-134219P	P	19990514
US	1999-134[illegible]1P	P	1999051[illegible]
US	1999-134[illegible]7P	P	1999051[illegible]
US	1999-134768P	P	19990518
US	1999-134941P	P	19990519
US	1999-135124P	P	19990520
US	1999-135[illegible]3P	P	1999052[illegible]
US	1999-13[illegible]4P	P	1999052[illegible]
US	[illegible]-[illegible]P	P	[illegible]
US	[illegible]-[illegible]P	P	[illegible]
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US	[illegible]-[illegible]P	P	[illegible]
US	1999-[illegible]P	P	1999[illegible]
US	1999-[illegible]P	P	1999[illegible]
US	1999-[illegible]P	P	1999[illegible]

AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays HYBRID SEED #38A1 and Arabidopsis thaliana (ecotype Wassilewskij), and polypeptides encoded thereby. The DNA mols. are useful for identifying a zea plant in whole, or in part, comprising in its genome a gene [illegible] promoter or [illegible] a gene in plant cells [illegible] transformation protocols, and for [illegible] gene in the Zea mays, in [illegible] tools for genetic mapping, for probing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present expt., but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 16 records supplemental to [illegible], as cited by the Lang no. If index entries required to fully index the document and publication system constraints.].

IT **302411-42-3 302411-43-4**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; sequence-determd. DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)

L11 ANSWER 21 OF 26 HCAPLUS COPYRIGHT [illegible] ACS
ACCESSION NUMBER: [illegible]
DOCUMENT NUMBER: 131:31656
TITLE: Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis
INVENTOR(S): Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.
PATENT ASSIGNEE(S): Ceres Inc., USA
SOURCE: Eur. Pat. Appl., 339 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 16
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1038878	A2	20000927	EP 2000-301439	20000224
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2300692	AA	20000825	CA 2000-2300692	20000224
CA 2302828	AA	20001006	CA 2000-2302828	20000406
EP 1260728	A2	20021127	EP 2002-[illegible]	20020614
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1054060	A2	20021211	EP 2000-[illegible]	20000517
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.: US 1999-121[illegible] P 19990225
US 1999-145919P P 19990727
US 1999-145951P P 19990728
US 1999-146340P P 19990802
US 1999-146344P P 19990802
US 1999-146348P P 19990802
US 1999-147[illegible] P 19990804
US 1999-147[illegible] P 19990804
US 1999-147[illegible] P 19990804
US 1999-147[illegible] P 19990806
US 1999-147[illegible] P 19990806

US [illegible]
US 1999-147416P P 1999[illegible]
US 1999-147493P P 1999[illegible]
US 1999-147935P P 1999[illegible]
US 1999-148171P P 1999[illegible]
US 1999-148319P P 1999[illegible]
US [illegible]
US [illegible]
US [illegible]
US [illegible]
US 1999-[illegible]P P 1999[illegible]
US 1999-125788P P 1999[illegible]
US 1999-126264P P 19990325
US 1999-126785P P 19990329
US 1999-127462P P 19990401
US 1999-128234P P 19990406
US 1999-128714P P 19990408
US 1999-129845P P 19990416
US 1999-130077P P 19990419
US 1999-130449P P 19990421
US 1999-130510P P 19990423
US 1999-130891P P 19990423
US 1999-131449P P 19990428
US 1999-132048P P 19990430
US 1999-132407P P 19990430
US 1999-132484P P 19990504
US [illegible]
US [illegible]
US 1999-132487P P 1999[illegible]
US 1999-132863P P 19990507
US 1999-134256P P 19990511
US 1999-134218P P 19990514
US 1999-134219P P 19990514
US 1999-134221P P 19990514
US 1999-134370P P 19990514
US 1999-134768P P 1999[illegible]
US 1999-134941P P 19990519
US 1999-135124P P 19990520
US 1999-135353P P 19990521
US 1999-135629P P 19990524
US 1999-136021P P 19990525
US 1999-136392P P 19990527
US 1999-136782P P 19990528
US 1999-137222P P 19990601
US [illegible]
US 1999-137802P P 1999[illegible]
US 1999-137724P P 1999[illegible]
US 1999-138194P P 19990608

AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA mols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence or as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present expt., but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CA133:2154, necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 301564-26-1 301564-27-2
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; sequence-detd. DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)

L11 ANSWER 22 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: [illegible] HCAPLUS
DOCUMENT NUMBER: 134:24[illegible]
TITLE: Cloning and expression of a gene encoding a putative chloroplast .omega.6 fatty acid desaturase of marine Chlamydomonas
AUTHOR(S): Miyasaka, Hitoshi; Tanaka, Satoshi; Kawamoto, Haruo
CORPORATE SOURCE: Tech. Res. Dept., The Kansai Electric Power Co., Inc., 11-20 Nakoji 3-chome, Amagasaki, Hyogo, [illegible], Japan
SOURCE: Plant Biotechnology (Tokyo, Japan), 17(4), 269-271
CODEN: PBIOFD; ISSN: 1342-4580
PUBLISHER: Japanese Society for Plant Cell and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A cDNA encoding putative chloroplast .omega.6 fatty acid desaturase was isolated from a cDNA library of marine Chlamydomonas sp. strain W-80. The mRNA level of this gene under various conditions of stress was examd. by northern blotting anal., and the transcript level was increased under a cold-stressed [4.degree.] condition.
IT 307998-10-3
RL: PRP (Properties)
(amino acid sequence; cloning and expression of a gene encoding a putative chloroplast .omega.6 fatty acid desaturase of marine Chlamydomonas)

L11 ANSWER 23 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:[illegible] HCAPLUS
DOCUMENT NUMBER: 1[illegible]
TITLE: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. [Erratum to document cited in CA129:77224]
AUTHOR(S): Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. V.; Eiglmeier, K.; Gas, S.; Barry, C. E., III; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, K.; Osborne, J.; Quail, M. A.; Rajandream, M.-A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, J.; Squares, R.; Squares, S.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. G.
CORPORATE SOURCE: Sanger Cent., Wellcome Trust Genome Campus, Hinxton, [illegible], UK
SOURCE: Nature (London, United Kingdom), [illegible], [illegible]
CODEN: NATUAS; ISSN: [illegible]
PUBLISHER: Macmillan Magazines
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Table 1 was published with some symbols missing; the correct version can be found at http://www.sanger.ac.uk and is given here. In Fig. 1, Rv1094c was incorrectly labeled as Rv1095 instead of fabD. Two of the genes in mycolyl transferase gene [illegible]: Rv3[illegible] was assigned as fbpA and not as fbpB, whereas Rv[illegible] was assigned as fbpB and not as fbpA. Introns. In [illegible], Rv[illegible] is now designated fbpB. The sequence of Rv1484 from M. bovis BCG-Pasteur

presented in Fig. [illegible] was incorrect and the [illegible]
relative humans [illegible].

IT 208786-02-1
RL: PRP (Properties)
deciphering the [illegible] of Mycobacterium tuberculosis from the complete genome sequence (Erratum)

L11 ANSWER 24 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:61353 HCAPLUS
DOCUMENT NUMBER: [illegible]
TITLE: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
AUTHOR(S): Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. V.; Eiglmeier, K.; Gas, S.; Barry, C. E., III.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; Mclean, J.; Moule, S.; Murphy, L.; Oliver, K.; Osborne, J.; Quail, M. A.; Rajandream, M.-A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, J.; Squares, R.; Squares, S.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. G.
CORPORATE SOURCE: Sanger Cent., Wellcome Trust Genome Campus, Hinxton, CB10 1SA, UK
SOURCE: Nature (London) [illegible], 393(6685), 537-544
CODEN: NATURAS; ISSN: [illegible]
PUBLISHER: Macmillan Magazines
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Countless millions of people have died from tuberculosis, a chronic infectious disease caused by the tubercle bacillus. The complete genome sequence of the best-characterized strain of Mycobacterium tuberculosis, H37Rv, was detd. and analyzed in order to improve our understanding of the biol. of this slow-growing pathogen and to help the conception of new prophylactic and therapeutic interventions. The genome comprises 4,411,529 base pairs, contains around 4000 genes, and has a very high G+C content that is reflected in the biased amino acid content of the proteins. M. tuberculosis differs radically from other bacteria in that a very large portion of its coding capacity is devoted to the prodn. of enzymes involved in lipogenesis and lipolysis, and to 2 new families of glycine-rich proteins with a repetitive structure that may represent a source of antigenic variation.
IT 208786-02-1
RL: PRP (Properties)
amino acid sequence; deciphering the [illegible] of Mycobacterium tuberculosis from the complete genome sequence
REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 25 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:61353 HCAPLUS
DOCUMENT NUMBER: [illegible]
TITLE: [illegible] of a gene for chloroplast [illegible] desaturase in a green alga, Chlamydomonas reinhardtii
AUTHOR(S): Sato, Norihiro; Fujiwara, Shoko; Kawaguchi, Akihiko; Tsuzuki, Mikio
CORPORATE SOURCE: School of Life Science, Tokyo University of Pharmacy and Life Science, Tokyo, 192-03, Japan
SOURCE: Journal of Biochemistry (Tokyo) [illegible], [illegible], [illegible]
[illegible]
CODEN: [illegible]; ISSN: [illegible]
PUBLISHER: [illegible]

DOCUMENT TYPE: Journal
LANGUAGE: English

AB A gene for chloroplast .omega.6 desaturase, which catalyzes the desatn. of monoenoic to dienoic acids in chloroplasts, was isolated from Chlamydomonas reinhardtii. Because transformation of [illegible] reaction was first performed with [illegible] .DELTA.12 desaturase of Synechocystis, using C. reinhardtii [illegible] DNA. An amplified DNA fragment of 1.7 kb, coding a frame for a protein homologous to these desaturases, was used as a probe for screening cDNA and genomic DNA libraries of C. reinhardtii. The cDNA clone of 2.2 kb obtained contained an open reading frame encoding a protein of 424 amino acids with a putative mol. mass of 48.4 kDa, the amino acid sequence of which showed 46-51% homol. to those of higher plant plastid .omega.6 and cyanobacterial .DELTA.12 desaturases. Introduction of the cloned genomic counterpart of this cDNA, designated as des6, into a Chlamydomonas mutant with defects in chloroplast .omega.6 desatn. and in the activities of photosystems I and II (PSI and PSII) complemented the desatn. mutation, indicating that the des6 gene codes for chloroplast .omega.6 desaturase. The complemented strains did not recover from the photosynthetic lesions, but showed lower PSII activity at 45.degree. than the desatn. mutant, proving that the photosynthetic lesions in hf-9 are not caused by the desatn. mutation, and that the lowered unsatn. level of chloroplast lipids in the mutant is responsible for the expression of this high temp. of PSII activity, one of the thylakoid membrane functions.

IT **204279-00-5**
RL: BSU (Biological study, unclassified ; PRP (Properties); BIOL (Biological study)
(amino acid sequence; cloning and sequence of gene des6 for chloroplast .omega.6 desaturase of a green alga, Chlamydomonas reinhardtii)

L11 ANSWER 26 OF 26 HCAPLUS COPYRIGHT 2013 ACS
ACCESSION NUMBER: 1996:910841 HCAPLUS
DOCUMENT NUMBER: 124:47157
TITLE: Identification and functional analysis of the transfer region of plasmid pMEA300 of the methylotrophic actinomycete Amycolatopsis methanolica
AUTHOR(S): Vrijbloed, J. W.; van der Put, N. M. J.; Dijkhuizen, L.
CORPORATE SOURCE: Dep. Microbiology, Univ. Groningen, Haren, 9751, Neth.
SOURCE: Journal of Bacteriology (1996), 177(22), 6499-505
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Amycolatopsis methanolica contains a 13.3-kb plasmid (pMEA300) that is present either as an integrated element or as an autonomously replicating plasmid. Conjugational transfer of pMEA300 results in pore formation, zones of growth inhibition that [illegible] donor cells normally [illegible] cells. A 6.2-kb pMEA300 DNA region specifying the functions of conjugation and pore formation was sequenced, revealing 10 open reading frames. This is the first sequence of the transfer region of a plasmid from a nonstreptomycete actinomycete. No clear similarities were found between the deduced sequences of the 10 putative Tra proteins of pMEA300 and those of Streptomyces plasmids. All Tra proteins of pMEA300 thus may represent unfamiliar types. A detailed mutational anal. showed that at least four [illegible] proteins, TraA (31,000 Da), TraH (31,000 Da), TraI (31,000 Da), and TraJ (31,000 Da), are required for efficient transfer of pMEA300. Their disruption resulted in a clear redn. in the conjugational transfer frequencies, ranging from 10.2 times 10[1]-fold (TraJ) to 10.2 times 10[4]-fold (TraI), and in reduced pore sizes. At least two putative proteins, TraA (31,000 Da) and TraB (31,000 Da), were shown to be

[illegible] pMEA311-encoded DNA plasmid [illegible] intramembrane region was used.

IT 171885-85-1
RL: BPR (Biological process)
amino acid sequence, identification and functional anal. of transfer region of plasmid pMEA311 in methylotrophic actinomycete Amycolatopsis methanolica

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http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

=>
=>

=>
=> d .seq l3 1-38

L3 ANSWER 1 OF 38 REGISTRY COPYRIGHT 2013 ACS
RN 487379-77-1 REGISTRY
CN GenBank BAA83822 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BAA83822 (Translated from: GenBank AB031646)
SQL 421

SEQ 1 QENMKDWNGY TGALFKFPLG TPLKLMASTG HRAINHFDLN KYTEKQRPRV
=======
HITS AT: 232-237

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L3 ANSWER 2 OF 38 REGISTRY COPYRIGHT 2013 ACS
RN 457323-42-6 REGISTRY
CN GenBank BAB11133 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BAB11133 (Translated from: GenBank AB016844)
SQL 254

SEQ 51 SAVLPKPLEN LVPLIYVLIF TRRAVVPPWV LSVPLWGLAL

HITS AT: 76-

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L3 ANSWER 3 OF 34 REGISTRY COPYRIGHT 2011 ACS
RN [illegible] REGISTRY
CN GenBank AAN[illegible] (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAN[illegible] (Translated from: GenBank AY[illegible])
SQL [illegible]

SEQ 1 MGWSAIVLFL ASWHGANAMT ALPSAKPKIS PTLAPRLVI [illegible]
= [illegible]
HITS AT: 1-18

L3 ANSWER 4 OF 34 REGISTRY COPYRIGHT 2011 ACS
RN 4[illegible]-[illegible] REGISTRY
CN GenBank AAM[illegible] (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AAM[illegible] (Translated from: GenBank AY186161)
SQL 326

SEQ 111 ALLSSKFTKE EIAFTVVTSG SPLTNSLAKL TESPYVLSID WARWHFFWID
======
HITS AT: 141-146

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L3 ANSWER 5 OF 34 REGISTRY COPYRIGHT 2011 ACS
RN 481335-47-1 REGISTRY
CN GenBank CAC42[illegible] (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank CAC42[illegible] (Translated from: GenBank AX114991)
SQL 170

SEQ 51 KTLMELGNGP LRPWASIGHW LLKHFDLSKY RESEKPRVKI SLAAVFAFMA
= =====
HITS AT: 71-75

L3 ANSWER 6 OF 34 REGISTRY COPYRIGHT 2003 ACS
RN 4[illegible]-[illegible] REGISTRY
CN Protein (Human clone HFIEC13) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 104: PN: US20020165137 SEQID: 104 claimed protein
NTE

type	------ location ------		description
uncommon	Aaa-9[illegible]	-	-
uncommon	Aaa-9[illegible]	-	-
uncommon	Aaa-11[illegible]	-	-
uncommon	Aaa-141	-	-
uncommon	Aaa-14[illegible]	-	-

SQL 175

SEQ 51 AQFLRASHFA RTTSCNTAMH PQISKFAQLA SVSPYFFNIS VSLPFNFMSA
[illegible]
HITS AT: 71-71

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: [illegible]

L3 ANSWER 7 OF 34 REGISTRY COPYRIGHT 2011 ACS

RN [illegible] REGISTRY
CN Protein (Mycobacterium tuberculosis strain [illegible] gene MT1683) (9CI) (CA
    INDEX NAME)
OTHER NAMES:
CN GenBank AE018014-derived protein 41 [illegible]
SQL 297

SEQ   1 MITAIMPEVT PVAPSSSLLA MAPHTNIIWH PDHALNLLSI IDAPLLAAQC
                                          ====== =

HITS AT: [illegible]

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: [illegible]

L3 ANSWER [illegible] OF 38 REGISTRY [illegible]
RN 440301-94-8 REGISTRY
CN Protein (Methanosarcina mazei strain Gö1 gene MM0190) (9CI) (CA INDEX
    NAME)
OTHER NAMES:
CN GenBank AE013474-derived protein GI [illegible]
SQL 276

SEQ   151 LQSRYTFFMA SLIFGILWGL WHFFLIFIKD MYQYRIFHEN IWIAVNFFVG
                               === ===

HITS AT: 168-173

REFERENCE 1: [illegible]

L3 ANSWER 9 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 437141-30-5 REGISTRY
CN 6-Phosphogluconolactonase (Arabidopsis thaliana clone RAFL05-06-O12
    (RC98ee) gene At5g24400) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF370305-derived protein GI 13878085
SQL 219

SEQ   51 GGSLIKSLRK LVESPYYDSI DWARKHFIWY DERIVIKNHD DSNYKLAYDS
                                   =====

HITS AT: [illegible]

REFERENCE 1: [illegible]

L3 ANSWER 10 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 437115-91-8 REGISTRY
CN Protein (human clone US20020049769-SEQID-44744 exon-encoded fragment)
    (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4708: PN: US20020049769 SEQID: 44744 claimed protein
SQL 34

SEQ   1 NIIQLLEGEI HHGAWQNANR AWHPKPILME SIEGLR
                               == ====

HITS AT: [illegible]

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: [illegible]

L3 ANSWER 11 OF 38 REGISTRY [illegible]
RN [illegible] REGISTRY
CN L-Arginine, L-[illegible]

histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-methionyl-L-.alpha.-glutamyl-L-seryl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-leucyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 98: PN: WO0157275 SEQID: 33858 claimed protein
CN Protein (human brain clone WO0157275-SEQID-33858 exon-encoded fragment)
SQL 36

SEQ 1 NIIQLLEGFI HHGAWQNAWR AWHFKFILME SIEGLR
== ====
HITS AT: 19-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:351357

L3 ANSWER 12 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 41[illegible]969-90-5 REGISTRY
CN L-Arginine, L-asparaginyl-L-isoleucyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-leucyl-L-.alpha.-glutamylglycyl-L-phenylalanyl-L-isoleucyl-L-histidyl-L-histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-methionyl-L-.alpha.-glutamyl-L-seryl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-leucyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 35[illegible]: PN: WO0157275 SEQID: 33858 claimed protein
CN Protein (human brain clone WO0157275-SEQID-33858 exon-encoded fragment)
SQL 36

SEQ 1 NIIQLLEGFI HHGAWQNAWR AWHFKFILME SIEGLR
== ====
HITS AT: 19-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:320295

L3 ANSWER 13 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 40[illegible]874-66-6 REGISTRY
CN Protein (Methanosarcina acetivorans strain C2A gene MA1162) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AE010783-derived protein GI 19914997
SQL 289

SEQ 151 LQSRHTFFTA SIFFSILWSL WHFPLIFVNN MYQYEIFHEN VWYAVNFFVS
=== ===
HITS AT: 169-173

REFERENCE 1: 136:[illegible]

L3 ANSWER 14 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 40[illegible]671-83-4 REGISTRY
CN L-Arginine, L-asparaginyl-L-isoleucyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-leucyl-L-.alpha.-glutamylglycyl-L-phenylalanyl-L-isoleucyl-L-histidyl-L-histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-methionyl-L-.alpha.-glutamyl-L-seryl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:
CN 855: PN: WO0157277 SEQID: 3481 claimed protein
CN Protein (human bone marrow [illegible]) [illegible]
SQL 84

SEQ 1 MTLLLEGFI HHGAW,MAWR AWHPKFILME SIELR
== ==

HITS AT: 19-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:[illegible]

L3 ANSWER 16 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 410957-73-8 REGISTRY
CN Protein (human fetal liver clone WO0157277-SEQID-3351A exon-encoded fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 528: PN: WO0157277 SEQID: 3351 A claimed protein
SQL 84

SEQ 1 MTLLLEGFI HHGAW,MAWR AWHPKFILME SIELR
== ==

HITS AT: 19-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:196269

L3 ANSWER 16 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 400696-91-5 REGISTRY
CN Secretory protein (human clone HNNBM45 53-amino acid precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 96: PN: WO0216390 SEQID: 98 claimed protein
NTE

type	------ location ------		annotation
unsure	Ala-51	-	-

SQL 53

SEQ 1 MVFLSHLPGT NRLFLLLALL WAQWHPGTMP APAWTDPGIP DNYLQAYLSI
=== =

HITS AT: 21-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:190341

L3 ANSWER 17 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 400664-75-7 REGISTRY
CN L-Arginine, L-asparaginyl-L-isoleucyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-leucyl-L-.alpha.-glutamylglycyl-L-phenylalanyl-L-isoleucyl-L-histidyl-L-histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-.alpha.-glutamyl-L-tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-.alpha.-glutamyl-L-serinyl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-leucyl- [illegible] (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 107: PN: WO0157277 SEQID: 3481 claimed protein

CN Protein human placenta cDNA Mus M. [redacted]-SE_II-5429A exon-encoded fragment,
SQL 36

SEQ 1 MIIQLLFGFI HHGAVQMAHA ANHFKFILME SIEGLR
                    == ====
HITS AT: 14-24

RELATED CE,TEXTBK AVAILABLE WITH CE_LINK

REFERENCE 1: [redacted]

L3 ANSWER 18 OF 34 REGISTRY COPYRIGHT 2003 ACS
RN 394342-68-2 REGISTRY
CN SPERMIDINE SYNTHASE TRANSMEMBRANE PROTEIN (Ralstonia solanacearum strain GMI1000 gene speE1) (9CI) (CA INDEX NAME
OTHER NAMES:
CN GenBank AL646084-derived protein [redacted]
SQL 511

SEQ 151 VSLLFPLVLA PRLGLVRTGF LFGLCNTAIA VWTLWHFRAE LGLSARLRGA
                                                 ======
HITS AT: 162-167

REFERENCE 1: 136:145954

L3 ANSWER 19 OF 34 REGISTRY COPYRIGHT 2003 ACS
RN 394342-70-2 REGISTRY
CN SPERMIDINE SYNTHASE PROTEIN (Ralstonia solanacearum strain GMI1000 gene speE2) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AL646084-derived protein GI 17431774
SQL 505

SEQ 151 LVSRVLTFDY LGALAVSLLP PLVLARLGL VRTGFLFGLC NTAIAVWTLW
                                                 ====
       201 HFTAELSLSA RLRGAMAWSA GMTMALLAS PAASGRITHW SERALPGDEI
           ==
HITS AT: 197-202

REFERENCE 1: 136:145954

L3 ANSWER 20 OF 34 REGISTRY COPYRIGHT 2003 ACS
RN 364873-96-4 REGISTRY
CN Musculoskeletal-associated antigen (human clone HFIEC13-883185 fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1147: PN: WO0155367 SEQID: 1155 claimed protein
NTE
---
 type ------ Location ------ Modification
---
uncommon Ala-30 - -
uncommon Ala-95 - -
uncommon Ala-104 - -
uncommon Ala-141 - -
uncommon Ala-145 - -

SQL 147

SEQ 31 A,RLRA HRA RAT WGQWH PSAVW GGLA TTAVTLTTG VA,PPPLA
                  ==== =
HITS AT: 46-51

RELATED SEQUENCES AVAILABLE WITH CN,[illegible]

REFERENCE 1: [illegible]

L3 ANSWER 21 OF 39 REGISTRY COPYRIGHT 2013 ACS
RN [illegible]-3 REGISTRY
CN 176: PN: WO0157187 SEQID: 176 claimed protein, 99% [illegible] NA INDEX NAME
NTE

type	location	description
unknown	A11-61	-

SQL 53

SEQ 1 MTFLSHLFST KRLFLLLALI WASWHFSYMG ADAWTDPGIP DRYLQAYLSI

HITS AT: 21-26

RELATED SEQUENCES AVAILABLE WITH CN,[illegible]

REFERENCE 1: 135:385111

L3 ANSWER 22 OF 39 REGISTRY COPYRIGHT 2013 ACS
RN 354113-34-1 REGISTRY
CN L-Phenylalanine, L-methionyl-L-glutaminyl-L-leucyl-L-prolyl-L-isoleucyl-L-tryptophyl-L-leucyl-L-histidyl-L-leucyl-L-seryl-L-seryl-L-tyrosyl-L-isoleucyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-arginyl-L-threonyl-L-methionyl-L-.alpha.-glutamyl-L-leucyl-L-isoleucyl-L-seryl-L-alanyl-L-seryl-L-valyl-L-leucyl-L-seryl-L-valyl-L-.alpha.-aspartyl-L-leucyl-L-leucyl-L-isoleucyl-L-leucylglycyl-L-leucyl-L-leucyl-L-tyrosyl-L-lysyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 176: PN: WO0157187 SEQID: 176 claimed protein
CN Bone marrow-specific protein (human clone WO0157187-SEQID-176 precursor)
SQL 43

SEQ 1 MQLPIWLHLS SYIWLIWHFR TMELISASYL SVDLLILSLL YKF

HITS AT: 14-19

REFERENCE 1: 135:163431

L3 ANSWER 23 OF 39 REGISTRY COPYRIGHT 2013 ACS
RN [illegible]-3 REGISTRY
CN Bone marrow-specific protein (human clone WO0157187-SEQID-364 contig-encoded precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 361: PN: WO0157187 SEQID: 364 claimed protein
NTE

type	location	description
unknown	A11-33	-

SQL 96

SEQ 31 PWHMQLPIWL HLSSYIWLIW HFRTMELISA SVLSVDLLIL SLLYKF

HITS AT: [illegible]

REFERENCE 1: [illegible]

L4 ANSWER 24 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN [illegible]-8 REGISTRY
CN Protein, human clone HFTEN1F1 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 84: PN: WO0168644 SEQID: 174 claimed protein
NTE

type	------ location ------	description
UNCERTAIN	Ala1-Pro2	-
UNCERTAIN	Ala1-Val4	-
UNCERTAIN	Ala1-Leu7	-
UNCERTAIN	Ala1-Val11	-
UNCERTAIN	Ala1-Val14	-

SQL 178

SEQ 51 AQRLRAGHRA GGTGCWGAWH FSGSWRGSLA SVGPVPPNVS VSQPFXFXSA
=====

HITS AT: 66-71

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:163414

L3 ANSWER 25 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 343286-49-7 REGISTRY
CN Protein LMRP (Physcomitrella patens clone 55_pK5_b04fwd lipid metabolism-related) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 241: PN: WO0194541 SEQID: 174 claimed protein
SQL 178

SEQ 51 PATKTLMELG MGPLRPWASI GHWLLWHFTL SKYRESEKPR VKISLLAVPA
=======

HITS AT: 73-78

REFERENCE 1: 135:14831

L3 ANSWER 26 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 307998-10-3 REGISTRY
CN Desaturase, fatty acid .omega.6-(Chlamydomonas strain W-80) (9CI) (CA INDEX NAME)
SQL 421

SEQ 201 QEKMKDWNGV TSALFKFFLG TPLKLWASVG HWAINHFDLN KYTEKQRPRV
=====

HITS AT: 231-237

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:2473

L3 ANSWER 27 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 302648-[illegible]-3 REGISTRY
CN Protein Arabidopsis thaliana clone [illegible] (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 869: PN: EP1033405 SEQID: [illegible] claimed protein
SQL 256

SEQ 51 PALLPKQLRA LVESPYFLLI LMAFMHFPWY TFFTVWWHH DSNTKLAITS
=====

HITS AT: 71-77

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 133:318297

L3 ANSWER 29 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 302645-68-4 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2141141) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 968: PN: EP1033405 SEQID: 60968 claimed protein
SQL 325

SEQ 101 ADLSDKFCKE RGAFTVVVSG GSLIKSLRKL VESPYVDSID WARWHFFWVD
======

HITS AT: 141-146

REFERENCE 1: 133:318297

L3 ANSWER 29 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 302411-43-4 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2113368) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 163: PN: EP1033405 SEQID: 55163 claimed protein
SQL 256

SEQ 51 GGSLIKSLRK LVESPYVDSI DWARWHFFWV DERVVPKNHD DSNYKLAYDS
======

HITS AT: 72-77

REFERENCE 1: 133:318296

L3 ANSWER 30 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 302411-42-3 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2113367) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 162: PN: EP1033405 SEQID: 55162 claimed protein
SQL 325

SEQ 101 ADLSDKFCKE RGAFTVVVSG GSLIKSLRKL VESPYVDSID WARWHFFWVD
======

HITS AT: 141-146

REFERENCE 1: 133:318296

L3 ANSWER 31 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 301564-27-2 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_1025180) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1596: PN: EP1033405 SEQID: 7409 claimed protein
SQL 256

SEQ 51 GGSLIKSLRK LVESPYVDSI DWARWHFFWV DERVVPKNHD DSNYKLAYDS
======

HITS AT: 72-77

REFERENCE 1: 133:306360

L3 ANSWER 32 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 301564-26-1 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_1025174) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1595: PN: EP1033405 SEQID: 7408 claimed protein
SQL 325

SEQ 1 [illegible]
HITS AT: 141-146

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 133:306836

L3 ANSWER 33 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN [illegible] REGISTRY
CN L-Phenylalanine, L-tryptophyl-L-valyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 13: PN: WO0044771 SEQID: 13 unclaimed sequence
SQL 6

SEQ 1 WVRAWHF
HITS AT: 1-6

REFERENCE 1: 133:146916

L3 ANSWER 34 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 286839-22-3 REGISTRY
CN L-Phenylalanine, L-tryptophyl-L-alanyl-L-arginyl-L-tryptophyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 12: PN: WO0044771 SEQID: 21 unclaimed sequence
SQL 6

SEQ 1 WARWHF
HITS AT: 1-6

REFERENCE 1: 133:146916

L3 ANSWER 35 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 286839-16-5 REGISTRY
CN L-Phenylalanine, L-tryptophyl-L-valyl-L-arginyl-L-tryptophyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2: PN: WO0044771 SEQID: 2 claimed sequence
SQL 6

SEQ 1 WVRWHF
HITS AT: 1-6

REFERENCE 1: 133:146916

L3 ANSWER 36 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN [illegible] REGISTRY
CN Protein PvlA + Myxococcus fulvus [illegible] NAME)
OTHER NAMES:
CN GenBank AAL21424-derived protein [illegible]
SQL 230

SEQ 1 MITRYNPRSS PVAASPHDR KRFHTWITMH PTHACNLPPI ITAGPLIADS

HITS AT: [illegible]

RELATED SEQUENCES AVAILABLE WITH SEQUENCE

REFERENCE 1: [illegible]

REFERENCE [illegible]

L3 ANSWER 37 OF 38 REGISTRY COPYRIGHT [illegible]
RN 204278-11-4 REGISTRY
CN Desaturase, fatty acid .omega.6- (Chlamydomonas reinhardtii clone pCD1 gene des6 reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN .omega.6 Desaturase (Chlamydomonas reinhardtii clone pCD1 gene des6 reduced)
CN [illegible]
SQL 484

SEQ 201 VTEADMAKWD STSAMLYKVF LGTPLKLWAS VGHWLVWHFD LNKYTPKQRT

HITS AT: 234-239

REFERENCE 1: 124:214987

L3 ANSWER 36 OF 38 REGISTRY COPYRIGHT [illegible]
RN 171885-85-1 REGISTRY
CN Protein TraH (plasmid pMEA300) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Protein TraH (Amycolatopsis methanolica plasmid pMEA300)
SQL 115

SEQ 1 MFTPEPKPTT DHTGQSTTEA VEARRAADLA IYTNAKYPTR TTQTVSWIGW

51 HFGELSGVVV PLGLGAAVWD GFYALSLLTA LGWAANELRL RRQQRAVRTR

HITS AT: 47-52

REFERENCE 1: 124:47157

```
=> fil hcaplus
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FILE COVERS 1907 - 13 Feb 2003  VOL 138 ISS 7
FILE LAST UPDATED: 12 Feb 2003  (20030212/ED)

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.


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=> d stat que l15
L1              1 SEA FILE=REGISTRY ABB=ON  PLU=ON  WVRWHF/SQSP
L2           1110 SEA FILE=REGISTRY ABB=ON  PLU=ON  W[GAILVSTKRHF]{GAILVSTKRHF}W[
                  GAILVSTKRHF]F/SQSP
L3             36 SEA FILE=REGISTRY ABB=ON  PLU=ON  W[GAILVSTKRHF]{GAILVSTKRHF}WHF/SQSP

L5              1 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L1
L6             27 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L3
L7              1 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L5 AND L6
L12            73 SEA FILE=REGISTRY ABB=ON  PLU=ON  L2 AND 3/EL=<50
L13            53 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L12
L14            16 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L13 NOT (2003 OR 2002)/PY
L15            17 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L14 NOT (L6 OR L7)


=>
=>

=> d ibib abs hitrn l15 1-17

L15  ANSWER 1 OF 17  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         2002:36295  HCAPLUS
DOCUMENT NUMBER:          136:1818
TITLE:                    Nucleic acids and their derivatives for
                          human tissues
INVENTOR(S):              Tang, Y. Tom; Liu, Yanhui; Ramnath, Radoje T.
PATENT ASSIGNEE(S):       Hyseq, Inc., USA
SOURCE:                   PCT Int. Appl., 147 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.        KIND  DATE            APPLICATION NO.   DATE
```

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001092523	A2	20011206	WO 2001-US16536	20010524
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2001070794	A5	20011212	AU 2001-70794	20010524
PRIORITY APPLN. INFO.:			US 2000-206126	A 20000524
			US 2000-577409	A 20000518

AB The present invention provides a collection or library of 13,901 nucleic acid contig sequences assembled from expressed sequence tag or cDNA libraries isolated mainly by sequencing by hybridization (SBH), std. PCR, Sanger sequencing techniques, and in some cases, sequences obtained from one or more public databases. The cDNA libraries are from human tissue sources and nearest neighbor sequence homologies are provided. The invention also relates to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. [This abstr. record is the fourth of four records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **432700-32-8**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acids and their encoded polypeptides from human tissues)

L15 ANSWER 2 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:896070 HCAPLUS
DOCUMENT NUMBER: 137:16519
TITLE: Human polypeptide fragments and their encoding cDNA polynucleotides
INVENTOR(S): Shimkets, Richard A.; Leach, Martin D.
PATENT ASSIGNEE(S): Curagen Corporation, USA
SOURCE: PCT Int. Appl., 1037 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001092523	A2	20011206	WO 2001-US16536	20010524
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

DK, DZ, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US [illegible]
US [illegible]
US [illegible]
WO [illegible]

AB The present invention provides 11,491 ORFX, novel human polypeptide fragments, as well as the 11,491 cDNA fragments encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivs., variants, mutants, or fragments of the ORFX polypeptides, polynucleotides, or antibodies. The invention addnl. provides methods in which the ORFX polypeptides, polynucleotides, and antibodies are used in detection and treatment of a broad range of pathol. states, as well as other uses. [This abstr. could not be fully enabled or complete due to limitations imposed by the large no. of index entries required, fully known for the present, and publication system constraints.].

IT **434378-63-9P**

RL: ANT (Analyte); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; human polypeptide fragments and their encoding cDNA polynucleotides)

L15 ANSWER 3 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:273192 HCAPLUS
DOCUMENT NUMBER: 133:295042
TITLE: Selection of an immunogenic and protective epitope of the PsaA protein of Streptococcus pneumoniae using a phage display library
AUTHOR(S): Srivastava, N.; Zeiler, J. L.; Smithson, S. L.; Carlone, G. M.; Ades, E. W.; Sampson, J. S.; Johnson, S. E.; Kieber-Emmons, T.; Westerink, M. A. J.
CORPORATE SOURCE: Department of Medicine, Medical College of Ohio, Toledo, OH, 43614, USA
SOURCE: Hybridoma (2000), 19(1), 23-31
CODEN: HYBRDY; ISSN: 0272-457X
PUBLISHER: Mary Ann Liebert, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB *Streptococcus pneumoniae* is an important pathogen that causes disease in young and elderly individuals. The currently available polysaccharide vaccines have limited efficacy in those age groups most susceptible to pneumococcal infections. This study focuses on mapping the epitopes of a surface protein of S. pneumoniae by biopanning a 15 mer phage display library using 5 different monoclonal antibodies (MAbs) against the Pneumococcal surface adhesin A (PsaA). PsaA is a component of the bacterial cell wall that is highly species specific and is involved in bacterial adherence and virulence. Biopanning of the phage display library reveals three distinct epitopes on the PsaA protein. The sequence homol. of these epitopes ranges from two to six amino acids when compared to the native PsaA protein type 2. Two of these epitopes have been evaluated for their immunogenicity in mice. The peptide selected by the MAbs 8G12, 6F6, and 1E7 is referred to as the consensus peptide and is immunogenic in mice. Optimal anti-PsaA response is obsd. in mice immunized with 5 .mu.g of the consensus peptide complexed to proteosomes in 1:1 ratio. The anti-PsaA response is significantly lower than the response to the intact protein. The peptide selected by [illegible] form is similarly protective in mice challenged intranasally with serotype 1 when compared to mice immunized with the native protein. These results show that the selected epitope of PsaA protein are immunogenic and protective in mice. These epitopes need to be evaluated further as alternatives to currently available vaccines.

IT **301300-56-1**

BL: BAC Biological activity or effector, except adverse ; BPN Biological study, unclassified ; THU Therapeutic use ; BIOL Biological study ; USES (Uses)
'PsaA protein of Streptococcus pneumoniae in vaccine against streptococcal infections'

REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RE. FORMAT

L16 ANSWER 4 OF 17 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:[illegible] HCAPLUS
DOCUMENT NUMBER: 131:124616
TITLE: Epitope peptides immunogenic against Streptococcus pneumoniae and their use in vaccines
INVENTOR(S): Carlone, George M.; Ades, Edwin W.; Sampson, Jacquelyn S.; Tharpe, Jean A.; Zeller, Joan Louise; Westerink, Maria Anna Julia
PATENT ASSIGNEE(S): The Government of the United States of America, represented by the Secretary, USA
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9945121	A1	19990910	WO 1999-US4326	19990226
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2326408	AA	19990910	CA 1999-2326408	19990226
AU 9927950	A1	19990920	AU 1999-27950	19990226
BR 9908476	A	20001205	BR 1999-8476	19990226
EP 1060249	A1	20001220	EP 1999-908543	19990226
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1998-[illegible]P P 19980302
WO 1999-US4326 W 19990226

AB Peptides are provided which immunospecifically bind to monoclonal antibodies specific for the 37-kDa pneumococcal surface adhesin A protein (PsaA) of Streptococcus pneumoniae of the invention, and that are immunogenic against Streptococcus pneumoniae infection. Also provided are vaccines comprising such immunogenic polypeptides, and methods of conferring protective immunity against Streptococcus pneumoniae infection by administering therapeutic regimens comprising the immunogenic peptides of the invention. Also provided are methods of detecting the presence of Streptococcus pneumoniae in a sample using antibodies or antigens, and methods of preventing and treating Streptococcus pneumoniae infection in a subject. In addn. a phage display method of identifying the sequence of a peptide potentially capable of eliciting protective immunity against a pathogenic microorganism is provided.

IT 241814-51-7P
BL: BIN Biochemical preparation ; PEP Properties ; THU Therapeutic use ; BIOL Biological study ; PREP Preparation ; USES Uses
(epitope peptides immunogenic against Streptococcus pneumoniae and their use in vaccines

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 5 OF 17 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:481741 HCAPLUS
DOCUMENT NUMBER: 129:76489
TITLE: Heparin- and sulfatide-binding peptides from the type I repeats of human thrombospondin and conjugates thereof for treatment of metastatic tumors and other neovascularization-related diseases
INVENTOR(S): Roberts, David D.; Browning, Philip J.; Bryant, Joseph L.; Inman, John K.; Fruttiger, Henry C.; Al., Sanghra
PATENT ASSIGNEE(S): United States Dept. of Health and Human Services, USA
SOURCE: U.S., 138 pp., Cont.-in-part of U. S. 215,046, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5770563	A	19980623	US 1995-487568	19950607
US 801812	A0	19921215	US 1991-801812	19911206
US 5357041	A	19941018		
US 6051549	A	20000418	US 1998-41119	19980311

PRIORITY APPLN. INFO.: US 1991-801812 A2 19911206
US 1994-215085 B2 19940321
US 1995-487568 A1 19950607

OTHER SOURCE(S): MARPAT 129:76489

AB This invention identifies a biol. active group of peptide sequences from Type I repeat units of the extracellular matrix protein, human thrombospondin-1, identical or homologous to the sequence, KRFKQDGGWSHWSPWSSC (SEQ ID NO:30). The biol. activities residing with the full sequences, portions thereof, and variants of the full [illegible] peptide sequences are disclosed. The [illegible] may be enhanced by covalently linking these peptides [illegible], preferably a branched, water-sol. polymer of low [illegible] mity and immunogenicity, such as polysucrose (Ficoll). The invention describes (1) a method for prepg. such conjugates, (2) the use of the defined peptides or their conjugates in blocking or modifying the action on cellular processes of heparin (e.g., proliferation, adhesion, motility, extravasation and neovascularization), sulfatides, related sulfated glycoconjugates, fibronectin, and basic fibroblast growth factor, involving malignant cell lines and normal endothelial cells. Use of the defined peptides, analogs or peptidomimetics and their conjugates for treatment of metastatic tumors, breast carcinomas, melanomas, Kaposi's sarcomas, hemangiomas, diabetic retinopathies, and various pathol. conditions dependent upon neovascularization is also disclosed.

IT 209457-55-6
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(heparin- and sulfatide-binding peptides from the type I repeats of human thrombospondin and conjugates thereof for treatment of metastatic tumors and other neovascularization-related diseases)

REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L18 ANSWER 6 OF 17 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:[illegible] HCAPLUS
DOCUMENT NUMBER: 129:[illegible]

TITLE: A region from the medium chain adaptor subunit (.mu.) recognizes leucine- and tyrosine-based sorting signals
AUTHOR(S): Bremnes, Torill; Lauvrak, Vigdis; Lindqvist, Bjorn; Bakke, Oddmund
CORPORATE SOURCE: Dep. Molecular Cell Biol., Inst. Basic Med. Sci., Univ. Oslo, Oslo, N-0317, Norway
SOURCE: Journal of Biological Chemistry (1998), 273(5), 2798-2805. CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Tyrosine-based sorting signals in the cytosolic tails of membrane proteins have been found to bind directly to the medium chain subunit (.mu.) of the adaptor complexes AP-1 and AP-2. For the leucine-based signals, an interaction with AP-1 and AP-2 has been reported, but no specific interacting subunit has been demonstrated. After searching for mols. interacting with the leucine-based sorting signals within the cytosolic tail of the major histocompatibility complex class II-assocd. invariant chain using a phage display approach, we identified phage clones with homol. to a conserved region of the AP-1 and AP-2 .mu. chains. To investigate the relevance of these findings, we have expressed regions of mouse .mu.1 and .mu.2 chains on phage gene product III and investigated the binding to tail sequences from various transmembrane proteins with known endosomal targeting signals. Enzyme-linked immunosorbent binding assays showed that these phages specifically recognized peptides contg. functional leucine- and tyrosine-based sorting signals, suggesting that these regions of the .mu.1 and .mu.2 chains interact with both types of sorting signals.

IT **208192-30-7P**
RL: BPN (Biosynthetic preparation); BIM (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation); PROC (Process)
(region from medium chain adaptor subunit (.mu.) of AP-1 and AP-2 recognizes leucine- and tyrosine-based sorting signals)

REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 7 OF 17 HCAPLUS COPYRIGHT 2013 ACS
ACCESSION NUMBER: 1998:11596 HCAPLUS
DOCUMENT NUMBER: 128:110913
TITLE: Amino acids within residues 181-200 of the nicotinic acetylcholine receptor .alpha.1 subunit involved in nicotine binding
AUTHOR(S): Lentz, Thomas L.; Chaturvedi, Vijaya; Conti-Fine, Bianca M.
CORPORATE SOURCE: Department of Cell Biology, Yale University [illegible], New Haven, CT, [illegible], USA
SOURCE: Biochemical Pharmacology (1997), [illegible], 341-347. CODEN: BCPCA6; ISSN: [illegible]
PUBLISHER: Elsevier Science Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Structural determinants of L-[3H]nicotine binding to the sequence flanking Cys 192 and Cys 193 of the Torpedo acetylcholine receptor .alpha.1 subunit were investigated using synthetic peptides (residues 181-[illegible]) and fusion proteins (residues [illegible]). Nicotine binding at a single conc. (50 nM) was compared with 21 peptides and fusion proteins in which individual amino acids at positions 181-200 were substituted. Substitution of Lys 189, Tyr 190, Cys 192, Cys 193, Thr 194, and Tyr 198 resulted in the greatest redn. in nicotine binding. Equil. binding of [3H]nicotine to peptide 181-200 revealed a binding component with an apparent Kd of 1.2

.mu.M. Substitution of Lys [illegible], Arg [illegible], Tyr [illegible], Tyr [illegible], Tyr 193, and Tyr 198 resulted in a significant redn. in affinity. Affinity was not affected significantly by substitution of Arg 182, Lys 183 (with Gly or Arg), Val 185, Tyr 189, Pro 194, Asp 195, Thr 196, and Asp 201. It is concluded that Lys [illegible], His 186, Tyr 190, Cys 192, Cys 193, and Tyr 198 play the greatest role in nicotinic binding to residues 181-200 of the .alpha.1 subunit. Previous studies have implicated Tyr [illegible], Lys 145, Lys 146, and Tyr 147 in agonist binding to the acetylcholine receptor. These results confirm a role for these residues and also demonstrate a function for Lys [illegible] and His 186 in nicotine binding.

IT 201529-09-1
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(181-200 nicotinic receptor .alpha.1-subunit mutant; nicotinic acetylcholine receptor .alpha.1 subunit residues 181-200 in nicotine binding)

L15 ANSWER 8 OF 17 HCAPLUS COPYRIGHT [illegible] ACS
ACCESSION NUMBER: [illegible]:53381 HCAPLUS
DOCUMENT NUMBER: 124:114269
TITLE: Isolation and characterization of antibodies which specifically recognize the peptide encoded by exon 7 (v2) of the human CD44 gene
AUTHOR(S): Borgya, A; Woodman, A; Sugiyama, M; Donie, F; Kopetzki, E.; Matsumura, Y; Tarin, D
CORPORATE SOURCE: Boehringer Mannheim GmbH, Penzberg, D-82371, Germany
SOURCE: Clinical Molecular Pathology (1995), 48(5), M241-M250
CODEN: CMPAFI; ISSN: 1355-2910
PUBLISHER: BMJ Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Exon 7 of the human CD44 gene is overexpressed in many commonly occurring carcinomas. The aim of the study was to explore the diagnostic and therapeutic potential of this frequent abnormality. A new monoclonal antibody (mAb, M-23.6.1) and a polyclonal antibody (pAb, S-[illegible]) to the corresponding antigen were raised by immunizing mice and sheep, resp., with a specially constructed fusion protein HIV2 (gp32)-CD44 exon 7. Characterization of mAb M-23.6.1 by ELISA, Western blotting, immunocytochem., and FACS anal. confirmed that it specifically recognizes an epitope in the region between amino acids 14 and 33 of the peptide encoded by this exon. Western blotting expts. with two cell lines, BT111 and ZR75-1, known from RT-PCR data to be over-transcribing the exon, yielded a monospecific band of approx. 200 kDa, and immunocytochem. showed discrete membrane staining on the same cell lines. Fluorescent antibody cell sorting (FACS) revealed binding to greater than 90% of the cells of each of these lines. Specificity of recognition of the antigen was shown by inhibition of the precise immunoreactivity typically seen in ELISA and Western blots, by pre-incubation with synthetic exon 7 peptide or fragments of it. The new antibodies will be useful tools for the further anal. of abnormal CD44 isoforms and their clin. implications.
IT 172997-35-2
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(isolation and characterization of monoclonal antibody to peptide encoded by exon 7 of human CD44)

L15 ANSWER 9 OF 17 HCAPLUS COPYRIGHT [illegible] ACS
ACCESSION NUMBER: [illegible]:930102 HCAPLUS
DOCUMENT NUMBER: 118:230219
TITLE: [illegible]
[illegible]
[illegible]
AUTHOR(S): [illegible]

Fuchs, Sara
CORPORATE SOURCE: Dep. Chemical Immunology, Weizmann Inst. Science, Rehovot, 76100, Israel
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1991), 88(13), 5768-72
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: Natl Acad Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English.
AB The ligand binding site of the nicotinic acetylcholine receptor .alpha. is localized in the .alpha.-subunit within a region that includes Cys-192 and Cys-193. By analyzing the ligand binding of .alpha. in animal species that are resistant to .alpha.-neurotoxins, the authors have previously shown that for residues in this region, at positions 187, 189, 194, and 197, differ between animals sensitive (e.g., mouse) and resistant (e.g., mongoose and snake) to .alpha.-bungarotoxin (.alpha.-BTX). In the present study, the authors performed site-directed mutagenesis on a fragment of the mongoose AcChoR .alpha.-subunit (residues 122-205) and exchanged residues 187, 189, 194, and 197, either alone or in combination, with those present in the mouse .alpha.-subunit sequence. Only the mongoose fragment in which all four residues were mutated to the mouse ones exhibited .alpha.-BTX binding similar to that of the mouse fragment. The mongoose double mutation in which Leu-194 and His-197 were replaced with proline residues, which are present at these positions in the mouse AcChoR and in all other toxin binders, bound .alpha.-BTX to .apprxeq.60% of the level of binding exhibited by the mouse fragment. In addn., replacement of either Pro-194 or -197 in the mouse fragment with serine and histidine, resp., markedly decreased .alpha.-BTX binding. All other mutations resulted in no or just a small increase in .alpha.-BTX binding. These results have led the authors' to propose two subsites in the binding domain for .alpha.-BTX: the proline subsite, which includes Pro-194 and -197 and is crit. for .alpha.-BTX binding, and the arom. subsite, which includes amino acid residues 187 and 189 and dets. the extent of .alpha.-BTX binding.
IT **170662-94-9**, EARGWKHWVFYACCLTTHYLD **170662-98-3**, EARGWKHWVFYACCPTTHYLD **170662-99-4**, EARGWKHWVFYACCLTTPYLD **170663-00-0**, EARGWKHWVFYACCPTTPYLD
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(mongoose nicotinic receptor .alpha.-subunit binding domain mutant contg.; nicotinic receptor .alpha.-subunit .alpha.-bungarotoxin-binding domain arom. subsite and proline subsite)
IT **170663-01-1**, EARGWKHWVFYSCCPTTPYLD
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(mouse nicotinic receptor .alpha.-subunit binding domain contg.; nicotinic receptor .alpha.-subunit .alpha.-bungarotoxin-binding domain arom. subsite and proline subsite)
IT **170663-02-2**, EARGWKHWVFYSCWPTTPYLD **170663-03-3**, EARGWKHWVFYSCCSTTPYLD **170663-04-4**, EARGWKHWVFYSCCPTTHYLD
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(mouse nicotinic receptor .alpha.-subunit binding domain mutant contg.; nicotinic receptor .alpha.-subunit .alpha.-bungarotoxin-binding domain arom. subsite and proline subsite)

L16 ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2009 ACS
ACCESSION NUMBER: 1991:[illegible] HCAPLUS
DOCUMENT NUMBER: 115:[illegible]
TITLE: Profile of the regions of acetylcholine receptor .alpha. chain recognized by T-lymphocytes and by antibodies in MRL3-susceptible and non-susceptible mouse strains after different peripheral immunization

with the recep[illegible]
AUTHOR(S): Oshima, Minaki; Bachmair, Andreas P.; Atassi, M. Zouhair
CORPORATE SOURCE: Dep. Biochem., Baylor Coll. Med., Houston, TX, 77030, USA
SOURCE: Molecular Immunology (1994), 31(11), 803-14
CODEN: MOIMD5; ISSN: 0161-5890
DOCUMENT TYPE: Journal
LANGUAGE: English
AB SJL/J (B6) mice develop a neuromuscular disease, exptl. autoimmune myasthenia gravis (EAMG), after .gtoreq.2 immunizations with Torpedo californica acetylcholine receptor (AChR). To det. whether EAMG is related to recognition of particular region(s) on the main extracellular domain of the .alpha. chain (residues .alpha. 1-210) in prolonged immunization, the authors have examd. the differences in the antibody and T cell recognition profiles of B6 and SJL a strain that does not develop EAMG) mice after different periods and a no. of immunization with Torpedo AChR. In a given strain, antibodies and T cells recognized immunodominant regions, which may coincide or may be uniquely B cell or T cell determinants. Both B6 and SJL exhibited similar antibody recognition profiles after the 2nd and through the 4th immunizations with AChR. Major differences between the 2 strains were found in their T cell recognition of regions in the second part (residues 101-210) of the main extracellular domain of the .alpha. chain. T cells of SJL recognized consistently only one region (111-126) within this part of the .alpha. chain, whereas in B6, T cell recognition of 3 peptides (111-126, 146-162, and 182-198) and next neighbor regions to them persisted throughout the period. Of these 3 peptides, 146-162 was an immunodominant peptide unique to B6, as the other 2 peptides (111-126 and 182-198) were also recognized by either T cells or antibodies in SJL. To study the role of T cells recognizing region 146-162 in EAMG, a T cell line was generated against this region and the cells transferred into B6 mice followed by one Torpedo AChR injection. Enhancement of antibody prodn. toward .alpha. chain peptides was obsd. as an influence of T cell transfer compared to profiles at 1 wk. In addn., 1 out of 3 mice examd. showed signs of EAMG. These results suggest the importance of T cells recognizing residues 146-162 in EAMG. Thus, the presence of persistent T cell responses to the second half (residues 100-210) of the main extracellular domain of the .alpha. chain is assocd. with the development of EAMG in B6 mice, while absence of these responses in SJL mice may enable them to escape the disease. The presentation of the immunodominance of peptide 146-162 in the T cell repertoire in B6 is probably most important for the pathogenesis of EAMG in this strain.
IT **157960-63-9**
RL: BIOL (Biological study)
(in B- and T-cell epitope mapping on acetylcholine receptor .alpha. chain, autoimmune myasthenia gravis in relation to)

L15 ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:318925 HCAPLUS
DOCUMENT NUMBER: 121:318925
TITLE: Diagnosis of tumors by assay of CD44 splicing patterns
INVENTOR(S): Tarin, David; Matsumura, Yasuhiro
PATENT ASSIGNEE(S): ISIS Innovation Ltd., UK
SOURCE: PCT Int. Appl., 41 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9411[illegible]	A1	1994[illegible]	WO 1993-GB[illegible]	1993[illegible]
W: [illegible]				

RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
EP 611822 A1 19940817 EP 1993-916110 19930721
EP 611822 B1 19980617
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE
JP 07510731 T2 19951130 JP 1993-514274 19930721
IE 931651 B1 19940921
AT 166940 E 19980715 AT 1993-916110 19930721
NZ 248171 A1 19941027 NZ 1993-248171 19930721
W: CA, JP, NZ
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
CA 2140963 AA 19940217 CA 1993-2140963 19930721
EP 672130 A1 19950920 EP 1994-917249 19940114
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE
US 5631646 A 19970520 US 1995-422113 19950413
US 5879891 A 19990309 US 1995-422113 19950413
PRIORITY APPLN. INFO.: GB 1992-15447 19920721
GB 1993-01464 19930125
GB 1993-20103 19930921
WO 1993-GB1520 19930720
WO 1993-GB2394 19931122

AB There is marked over-expression of multiple spliced variants of the CD44 gene in tumor compared to counterpart normal tissue. This observation forms the basis of a method of diagnosing neoplasia by anal. of a sample of body tissue or body fluid or waste product. A new exon 6, of 129 bp, has been found and sequenced, and is claimed as such and for use in the diagnostic method. Samples of breast tumors were assayed for CD44 mRNA by reverse transcription/PCR using primers to detect hemopoietic CD44 followed by hybridization with a probe from exon 4. A no. of splice variants were found in neoplastic tissue that were absent from normal tissue, this was found in all patients tested. There was a difference in splice patterns between neoplastic and non-neoplastic diseased tissues (cystic disease). Similar results were found in colon cancer using biopsy and stool samples and in bladder cancer using urine samples for diagnosis.

IT **155216-25-4**
RL: PRP (Properties)
(amino acid sequence of, in neoplastic tissue, altered splicing patterns in neoplastic tissue in relation to)

L15 ANSWER 12 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1992:564026 HCAPLUS
DOCUMENT NUMBER: 117:164026
TITLE: Species- and subtype-specific recognition by antibody WF6 of a sequence segment forming an .alpha.-bungarotoxin binding site on the nicotinic acetylcholine receptor .alpha. subunit
AUTHOR(S): McLane, K. E.; Fritzen, M.; Wu, X.; Diethelm, B.; Maelicke, A.; Conti-Tronconi, B. M.
CORPORATE SOURCE: Coll. Biol. Sci., Univ. Minnesota, St. Paul, MN, 55108, USA
SOURCE: Journal of Receptor Research (1991), 11(8), 799-811
CODEN: JRREDM; ISSN: 0737-1111
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The monoclonal antibody WF6 competes with acetylcholine and .alpha.-bungarotoxin (.alpha.-BGT) for binding to the Torpedo nicotinic acetylcholine receptor (nAChR) .alpha.1 subunit. By using synthetic peptides corresponding to the complete Torpedo nAChR .alpha.1 subunit, the authors previously mapped a continuous epitope recognized by WF6, and the protetope for .alpha.-BGT, to the sequence segment .alpha.1(181-200). Single amino acid substitution analysis have been used as an initial approach to det. the critical amino acid(s) for WF6 and .alpha.-BGT binding. In the present study, the authors continue the anal. of the structural features of the WF6 epitope by comparing its cross-reactivity with

synthetic peptides ... nAChRs of different species, ... and .alpha.7 nAChR subtypes, ... results indicate that WF6 is able to cross-react with the muscle .alpha.1 subunits of different species by virtue of conservation of several bulky amino acid residues between positions 187-198 of the .alpha.1 subunit. These studies further define the essential structural features of the sequence segment .alpha.1 (181-200) required to form the epitope for WF6.

IT 133295-54-2 133322-53-9
RL: BIOL (Biological study)
(antibody ... binding site binding by, structure in relation to)

L16 ANSWER 13 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1991:223857 HCAPLUS
DOCUMENT NUMBER: 114:223857
TITLE: Structural determinants of .alpha.-bungarotoxin binding to the sequence segment 181-200 of the muscle nicotinic acetylcholine receptor .alpha. subunit: effects of synthetic cysteine substitutions and species-specific amino acid substitutions
AUTHOR(S): McLane, Kathryn E.; Wu, Xiadong; Diethelm, Brenda; Conti-Tronconi, Bianca M.
CORPORATE SOURCE: Coll. Biol. Sci., Univ. Minnesota, St. Paul, MN, 55108, USA
SOURCE: Biochemistry (1991), 30(20), 4925-34
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The sequence segment 181-200 of the Torpedo nicotinic acetylcholine receptor (nAChR) .alpha. subunit forms a binding site for .alpha.-bungarotoxin (.alpha.-BTX). Synthesis peptides corresponding to the homologous sequences of human, calf, mouse, chicken, frog, and cobra muscle nAChR .alpha.1 subunits were tested for their ability to bind 125I-.alpha.-BTX, and differences in .alpha.-BTX affinity were detd. by using soln. (IC50) and a solid-phase (Kd) assays. Panels of overlapping peptides corresponding to the complete .alpha.1 subunit of mouse and human were also tested for .alpha.-BTX binding, but other sequence segments forming the .alpha.-BTX site were not consistently detectable. The Torpedo .alpha.1(181-200) and the homologous frog and chicken peptides bound .alpha.-BTX with higher affinity (Kd .apprx. 1-2 .mu.M, IC50 .apprx. 1-2 .mu.M) than the human and calf peptides (Kd .apprx. 4-5 .mu.M, IC50 .apprx. 15 .mu.M). The mouse peptide bound .alpha.-BTX weakly when attached to a solid support (Kd .apprx. 8 .mu.M) but was effective in competing for 125I-.alpha.-BTX in soln. (IC50 .apprx. 1 .mu.M). The cobra nAChR .alpha.1-subunit peptide did not detectably bind .alpha.-BTX in either assay. Amino acid substitutions were correlated with .alpha.-BTX binding activity of peptides from different species. The role of a putative vicinal disulfide bond between cysteine-192 and -193, relative to the Torpedo sequence, was detd. by modifying the peptides with sulfhydryl reagents. Redn. and alkylation of the peptides decreased .alpha.-BTX binding, whereas oxidn. of the peptides had little effect. Modifications of the cysteine cystine residues of the cobra peptide failed to induce .alpha.-BTX binding activity. Thus, while the adjacent cysteines are likely to be involved in forming the toxin .alpha.1-subunit interface a vicinal disulfide bound was not required for .alpha.-BTX binding.

IT 133295-54-2P 133322-53-9P
RL: SPN (Synthetic preparation); PREP (Preparation)
(prepn. and .alpha.-bungarotoxin binding by, toxin binding site of nicotinic acetylcholine receptor .alpha. subunit in relation to)

IT 133295-53-1P
RL: SPN (Synthetic preparation); PREP (Preparation)

... paragraph ...

L16 ANSWER 14 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1990:524236 HCAPLUS
DOCUMENT NUMBER: 113:124236
TITLE: Interaction of a snake toxin receptor with and a synthetic peptide corresponding to .alpha.-subunit
AUTHOR(S): Bohner-Ely, Anne A.; Mishra, P. K.; Low, Barbara W.
CORPORATE SOURCE: Dep. Chem., Carnegie Mellon Univ., Pittsburgh, PA, 15213, USA
SOURCE: UCLA Symposia on Molecular and Cellular Biology, New Series (1989), 114 Biol. NMR Vol. Biol., 1-5. CODEN: USMBLQ; ISSN:
DOCUMENT TYPE: Journal
LANGUAGE: English
AB .alpha.-Cobratoxin and acetylcholine receptor .alpha.-subunit complementary binding domain peptide (residues 173-181) were studied by 1-D and 2-D NMR spectroscopy. A model for binding is proposed.
IT **114753-46-7**
RL: BIOL (Biological study)
(.alpha.-cobratoxin binding by, conformation in, NMR study of)

L16 ANSWER 15 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1988:516189 HCAPLUS
DOCUMENT NUMBER: 109:116189
TITLE: Binding of .alpha.-bungarotoxin to synthetic peptides corresponding to residues 173-204 of the .alpha. subunit of Torpedo, calf, and human acetylcholine receptor and restoration of high-affinity binding by sodium dodecyl sulfate
AUTHOR(S): Wilson, Paul T.; Lentz, Thomas L.
CORPORATE SOURCE: Sch. Med., Yale Univ., New Haven, CT, [illegible], USA
SOURCE: Biochemistry (1988), 27(19), [illegible]
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To investigate structure-function relations of a segment of the acetylcholine receptor .alpha. subunit, binding of .alpha.-bungarotoxin to synthetic peptides corresponding to residues 173-204 of Torpedo, calf, and human .alpha. subunits was compared using a solid-phase radioassay. The affinities of ^{125}I-labeled .alpha.-bungarotoxin for the calf and human peptides were 15- and 150-fold less, resp., than for the Torpedo peptide. On the basis of nonconservative substitutions in the calf and human sequences, arom. residues (Tyr-181, Trp-187, and Tyr-189) are important for the higher affinity binding of the Torpedo peptide. Substitution of neg. charged Glu-180 with uncharged Gln in the calf peptide did not significantly affect toxin binding, indicating Glu-180 alone does not comprise the anionic subsite on the receptor to which the cationic quaternary ammonium groups of cholinergic agents bind. d-Tubocurarine competed with toxin binding to the modified calf [illegible] with Ile-Glu-181 and Asp-195 present in Torpedo. Thus, the toxin binding subsite formed by another neg. charged residue or by 2 amino acid side chains. It is possible that the pos. charges on cholinergic ligands are countered by a neg. electrostatic potential provided by polar groups, such as the hydroxyl group of tyrosine, present in several residues in this region, and the neg. charges present on any of residues 178, 181, 187, 189, [illegible]. Equil. satn. binding of .alpha.-bungarotoxin with Torpedo peptide 173-204 revealed a major binding component with an apparent KD of 0.1 nM and a major component with a KD of 6 nM. In the presence of 0.1% SDS, 1 binding component with a KD of 0.2 nM was detected. This compares with an affinity of KD = 0.41 nM for toxin binding to native acetylcholine receptor in the solid-phase assay. SDS may stabilize a conformation of the peptide that is conducive to high-affinity binding.

IT 115826-29-4 115826-30-7
RL: BIOL (Biological study)
(bungarotoxin binding to, alkaline phosphatase binding in relation to

L15 ANSWER 16 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1988:4...71 HCAPLUS
DOCUMENT NUMBER: 110:2...1
TITLE: .alpha.-Toxin binding to acetylcholine receptor .alpha.179-191 peptides: intrinsic fluorescence studies
AUTHOR(S): Pedding, W.; Corfield, P. W. R.; Levinson, L. S.; Hashim, G. A.; Low, P. W.
CORPORATE SOURCE: Howard Hughes Inst., Columbia Univ., New York, NY, 10032, USA
SOURCE: FEBS Letters (1988), 231(1), 212-16
CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Interactions between 2 .alpha.-toxins and the synthetic peptides .alpha.179-191 from both calf and human acetylcholine receptor .alpha.-subunit sequences were studied by measurements of quenching of intrinsic fluorescence after toxin addn. Dissocn. consts. of .apprx.5 .times. 10-8M for binding of calf peptide by both .alpha.-cobrotoxin and erabutoxin a were estd. The binding of .alpha.-cobrotoxin to calf peptide, which leads to marked quenching of fluorescence intensity, is inhibited by a 1000 excess of acetylcholine. The human .alpha.179-191 peptide binds to .alpha.-cobrotoxin, but not, under comparable conditions, to erabutoxin a.
IT 114753-46-7P
RL: SPN (Synthetic preparation); PREP (Preparation)
(prepn. of, of calf acetylcholine receptor .alpha.-subunits, and .alpha.-toxins binding by)

L15 ANSWER 17 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1984:185956 HCAPLUS
DOCUMENT NUMBER: 100:185956
TITLE: A super active cyclic hexapeptide analog of somatostatin
AUTHOR(S): Veber, Daniel F.; Saperstein, Richard; Nutt, Ruth F.; Freidinger, Roger M.; Brady, Stephen F.; Curley, Paul; Perlow, Debra S.; Paleveda, William J.; Colton, C. Dylion; et al.
CORPORATE SOURCE: Merck Sharp and Dohme Res. Lab., West Point, PA, 19486, USA
SOURCE: Life Sciences (1984), 34(14), 1371-8
CODEN: LIFSAK; ISSN: 0024-3205
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Cyclo(N-methyl-Ala-Tyr-D-Trp-Lys-Val-Phe) (I) [81377-02-8] was 50-100-fold more potent than cyclic somatostatin [38916-34-6] for the inhibition of insulin [9004-10-8], glucagon [9007-92-5] and growth hormone [9002-72-6] release as revealed by structure-activity studies of cyclic hexapeptide analogs of somatostatin in rats. The hydroxyl group of tyrosine contributed a 10-fold enhancement to the potency. Potency was also correlated with hydrophobicity. I improved the control of postprandial hyperglycemia in diabetic animals when given in combination with insulin. The analog was quite stable in the blood and in the gastrointestinal tract, but the bioavailability after oral administration was only 1-3%. The biol. properties and long duration of I should allow clin. evaluation of the inhibition of glucagon release as an adjunct to insulin in the treatment of patients with diabetes.
IT 89808-58-2
RL: BIOL (Biological study)

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DICTIONARY FILE UPDATES: 12 FEB 2003 HIGHEST RN 469395-63-1

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Experimental and calculated property data are now available. See HELP
PROPERTIES for more information. See STNote 27, Searching Properties
in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

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=> s e4-e28 and l12
             1 114753-46-7/BI
               (114753-46-7/RN)
             1 133295-53-1/BI
               (133295-53-1/RN)
             1 133322-53-9/BI
               (133322-53-9/RN)
             1 115826-29-4/BI
               (115826-29-4/RN)
             1 115826-30-7/BI
               (115826-30-7/RN)
             1 133295-53-1/BI
               (133295-53-1/RN)
             1 [illegible]/BI
               ([illegible]/RN)
             1 157960-63-9/BI
               (157960-63-9/RN)
             1 170662-94-9/BI
               (170662-94-9/RN)
             1 170662-98-3/BI
               ([illegible]/RN)
             1 [illegible]/BI
               ([illegible]/RN)
             1 [illegible]/BI
               ([illegible]/RN)
             1 [illegible]/BI
               ([illegible]/RN)
             1 [illegible]/BI
               ([illegible]/RN)
             1 [illegible]/BI

[illegible]
1 [illegible]-4/BI
[illegible]
1 [illegible]
[illegible]
1 [illegible]
[illegible]
1 [illegible]
[illegible]
1 [illegible]
[illegible]
1 [illegible]
[illegible]
1 434378-63-9/BI
(434378-63-9/RN)
1 89808-58-2/BI
(89808-58-2/RN)

L16 25 (114753-46-7/BI OR 133208-64-[illegible]BI OR [illegible] OR [illegible]-12-4/BI OR 115826-30-7/BI OR [illegible] OR [illegible]-4/BI OR 157960-63-8/BI OR [illegible] OR [illegible]-4/BI OR [illegible]-4/BI OR [illegible] OR 170663-03-3/BI OR 170663-04-4/BI OR 170697-35-2/BI OR 203529-09-1/BI OR 208192-30-7/BI OR 209487-88-6/BI OR 241814-51-7/BI OR 301300-56-1/BI OR 432700-32-8/BI OR 434378-63-9/BI OR 89808-58-2/BI) AND L12

=> d .seq l16 1-25

L16 ANSWER 1 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN **434378-63-9** REGISTRY
CN L-Isoleucine, L-methionyl-L-seryl-L-tryptophyl-L-histidyl-L-seryl-L-tryptophyl-L-isoleucyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-.alpha.-glutamyl-L-isoleucyl-L-tyrosyl-L-leucyl-L-.alpha.-glutamyl-L-asparaginyl-L-threonyl-L-prolyl-L-cysteinyl-L-tyrosyl-L-lysyl-L-tyrosyl-L-.alpha.-glutamyl-L-threonyl-L-.alpha.-aspartyl-L-isoleucyl-L-leucyl-L-tyrosyl-L-isoleucyl-L-alanyl-L-seryl-L-phenylalanyl-L-.alpha.-aspartyl-L-phenylalanyl-L-seryl-L-arginyl-L-glutaminyl-L-isoleucyl-L-prolyl-L-seryl-L-threonyl-L-methionyl-L-arginyl-L-isoleucyl-L-seryl-L-valyl-L-tyrosyl-L-seryl-L-valyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3444: PN: WO01902503 SEQID: 8446 claimed protein
CN Protein (human clone WO01902503-SEQID-8446 fragment)
SQL **50**
RN **434378-63-9** REGISTRY
SQL **50**

SEQ 1 MSWHSWIFYS EIVLEMTFTY KYETPLLYIA VEPSRQIFR TKRISTVNVI
[illegible]
HITS AT: 3-8

REFERENCE 1: 137:1[illegible]

L16 ANSWER 2 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN **432700-32-8** REGISTRY
CN L-Threonine, L-glutaminyl-L-asparaginyl-L-leucyl-L-threonyl-L-alanyl-L-glutaminyl-L-.alpha.-aspartylglycyl-L-tryptophyl-L-glutaminyl-L-tryptophyl-L-lysyl-L-.alpha.-aspartyl-L-leucylglycyl-L-seryl-L-leucyl-L-glutaminyl-L-prolyl-L-prolyl-L-leucyl-L-prolyl-L-seryl-L-seryl-L-tryptophyl-L-.alpha.-aspartyl-L-tyrosyl-L-arginyl-L-arginyl-L-.alpha.-glutamyl-L-seryl-L-leucyl-

l-tyrosyl-l-prolyl-l-tryptophyl-l-threonyl-l-alanyl-l-tryptophyl-l-
is leucyl-l-phenylalanyl-l-tryptophyl-l-glycyl-l-arginyl-l-tyrosylglycyl-
l-phenylalanyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 5441: PN: WO2004[illegible] SEQID: 24445 claimed protein
CN Protein (human clone WO01644[illegible]-SEQID-24445 fragment)
SQL 47
RN 432700-32-8 REGISTRY
SQL 47

SEQ 1 [illegible]

HITS AT: 41-46

REFERENCE 1: 167:1511

L16 ANSWER 3 OF 25 REGISTRY [illegible]
RN 301300-56-1 REGISTRY
CN L-Tyrosine, N-(1-oxohexadecyl)-L-threonyl-L-valyl-L-arginyl-L-seryl-L-
valyl-L-prolyl-L-tryptophyl-L-threonyl-L-alanyl-L-tryptophyl-L-alanyl-L-
phenylalanyl-L-histidylglycyl- (9CI) (CA INDEX NAME)
MTE modified

type	------ location ------	description
modification	Thr-1 -	1-oxohexadecyl<Pal>

SQL 15
RN 301300-56-1 REGISTRY
SQL 15

SEQ 1 TVRSVPWTAW AFHGY

HITS AT: 7-12

REFERENCE 1: 139:249142

L16 ANSWER 4 OF 25 REGISTRY COPYRIGHT 2006 ACS
RN 241814-51-7 REGISTRY
CN L-Tyrosine, L-threonyl-L-valyl-L-seryl-L-arginyl-L-valyl-L-prolyl-L-
tryptophyl-L-threonyl-L-alanyl-L-tryptophyl-L-alanyl-L-phenylalanyl-L-
histidylglycyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: WO2004[illegible] SEQID: 5 claimed protein
SQL 15
RN 241814-51-7 REGISTRY
SQL 15

SEQ 1 TVSRVPWTAW AFHGY

HITS AT: 7-12

REFERENCE 1: 147:107804

REFERENCE 2: 136:117369

REFERENCE 3: 131:139716

L16 ANSWER 5 OF 25 REGISTRY [illegible]
RN 209457-55-6 REGISTRY
CN L-Serine, L-lysyl-L-arginyl-L-phenylalanyl-L-glycyl-L-leucyl-L-alpha-
aspartylglycylglycyl-L-tryptophyl-L-seryl-L-histidyl-L-tryptophyl-L-seryl-
L-phenylalanyl-L-tryptophyl-L-seryl- (9CI) (CA INDEX NAME)

SQL 17
RN 209457-55-6 REGISTRY
SQL 17

QY 1 [illegible]

HITS AT: [illegible]

REFERENCE 1: [illegible]

L16 ANSWER 6 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 208192-30-7 REGISTRY
CN Glycine, L-alanyl-L-.alpha.-aspartylglycyl-L-alanyl-L-tryptophyl-L-prolylalanyl-L-seryl-L-tryptophylglycyl-L-phenylalanyl-L-prolyl-L-glutaminyl-L-tryptophyl-L-tryptophylglycyl-L-alanyl-L-alanyl- (9CI) (CA INDEX NAME)
SQL 18
RN 208192-30-7 REGISTRY
SQL 18

SEQ 1 ADGAWPSWGF PQWWGAAG
[illegible]
HITS AT: [illegible]

REFERENCE 1: 129:91363

L16 ANSWER 7 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 201529-09-1 REGISTRY
CN L-Aspartic acid, L-tyrosyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-threonyl-L-cysteinyl-L-cysteinyl-L-prolyl-L-.alpha.-aspartyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 20
RN 201529-09-1 REGISTRY
SQL 20

SEQ 1 YRGWKHWVFY TCCPDTPYLD
[illegible]
HITS AT: [illegible]

REFERENCE 1: 128:110913

L16 ANSWER 8 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 172997-35-2 REGISTRY
CN L-Lysinamide, L-threonyl-L-tryptophyl-L-.alpha.-aspartyl-L-tryptophyl-L-phenylalanyl-L-seryl-L-tryptophyl-L-[illegible]
NTE modified

type	------ location ------		description
terminal mod.	Lys-15	-	C-terminal amide

SQL 15
RN 172997-35-2 REGISTRY
SQL 15

SEQ 1 TXTWPSWLFL PSPSK
[illegible]
HITS AT: [illegible]

REFERENCE 1: [illegible]

L16 ANSWER 12 OF 26 REGISTRY COPYRIGHT 2003 ACS
RN 170663-04-4 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-histidyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170663-04-4 REGISTRY
SQL 21

SEQ 1 EARGWKHWYP YSCCPTTHYL D
=======
HITS AT: 5-11

REFERENCE 1: 123:330219

L16 ANSWER 11 OF 26 REGISTRY COPYRIGHT 2003 ACS
RN 170663-03-3 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-cysteinyl-L-seryl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170663-03-3 REGISTRY
SQL 21

SEQ 1 EARGWKHWYP YSCCSTTPYL D
======
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 11 OF 26 REGISTRY COPYRIGHT 2003 ACS
RN 170663-02-2 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-tryptophyl-L-prolyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170663-02-2 REGISTRY
SQL 21

SEQ 1 EARGWKHWYP YSCWPTTPYL D
======
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 12 OF 26 REGISTRY COPYRIGHT 2003 ACS
RN 170663-01-1 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170663-01-1 REGISTRY
SQL 21

SEQ 1 EARGWKHWYP YSCWPTTPYL D
======
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 13 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170663-00-0 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170663-00-0 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YACPTTPYL 9
======
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 14 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170662-99-4 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-cysteinyl-L-leucyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170662-99-4 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YACPLTTPYL 9
======
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 15 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170662-98-3 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-histidyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170662-98-3 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YACPTTHYL 9
======
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 16 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170662-94-9 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-histidyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170662-94-9 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YACPLTTHYL 9
======
HITS AT: 5-10

[illegible]

REFERENCE 1: [illegible]

L16 ANSWER 17 OF 25 REGISTRY COPYRIGHT [illegible]
RN 157960-63-9 REGISTRY
CN L-Tyrosine, L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-prolyl- (9CI) (CA INDEX NAME)
SQL 17
RN 157960-63-9 REGISTRY
SQL 17

SEQ 1 RGWKHWIFYC CPTTPY
[illegible]
HITS AT: 3-8

REFERENCE 1: [illegible]

L16 ANSWER 18 OF 25 REGISTRY COPYRIGHT [illegible]
RN 155216-25-4 REGISTRY
CN L-Alanine, L-threonyl-L-leucyl-L-methionyl-L-seryl-L-threonyl-L-tryptophyl-L-alanyl-L-threonyl-L-alanyl-L-threonyl-L-lysyl-L-arginyl-L-glutaminyl-L-.alpha.-glutamyl-L-threonyl-L-tryptophyl-L-.alpha.-aspartyl-L-tryptophyl-L-phenylalanyl-L-seryl-L-tryptophyl-L-leucyl-L-phenylalanyl-L-leucyl-L-prolyl-L-seryl-L-.alpha.-glutamyl-L-seryl-L-lysyl-L-asparaginyl-L-histidyl-L-leucyl-L-histidyl-L-threonyl-L-threonyl-L-threonyl-L-glutaminyl-L-methionyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Antigen CD 44 (human exon 6)
SQL 43
RN 155216-25-4 REGISTRY
SQL 43

SEQ 1 TLMSTSATAT ETATKRQETW DWFSWLFLPS ESKNHLHTTT QMA
[illegible]
HITS AT: 22-27

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: [illegible]

L16 ANSWER 19 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 133322-53-9 REGISTRY
CN L-Aspartic acid, L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 20
RN 133322-53-9 REGISTRY
SQL 20

SEQ 1 ARGWKHWIFY SCCPTTPYLD
[illegible]
HITS AT: 4-9

REFERENCE 1: [illegible]

REFERENCE 2: [illegible]

L16 ANSWER 20 OF 25 REGISTRY [illegible]
RN 133295-54-2 REGISTRY
CN L-Aspartic acid, L-seryl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-

[illegible]ysteinyl-L-pr[illegible]lyl-L-seryl-L-thre[illegible]nyl-L-pr[illegible]yl-L-ty[illegible]syl-L-l[illegible]nyl- (9CI) (CA INDEX NAME)
SQL 20
RN 133295-54-2 REGISTRY
SQL 20

SEQ 1 [illegible]

HITS AT: 4-9

REFERENCE 1: 117:164016

REFERENCE 2: 114:223457

L16 ANSWER 21 OF 25 REGISTRY COPYRIGHT [illegible] ACS
RN 133295-53-1 REGISTRY
CN L-Serine, L-.alpha.-glutamyl-L-seryl-glycyl-L-.alpha.-glutamyl-L-tryptophyl-L-valyl-L-isoleucyl-L-lysyl-L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl- (9CI) (CA INDEX NAME)
SQL 20
RN 133295-53-1 REGISTRY
SQL 20

SEQ 1 ESGEWVIKEA EWKHWVFYYS
======
HITS AT: 13-18

REFERENCE 1: 114:223457

L16 ANSWER 22 OF 25 REGISTRY COPYRIGHT 2.13 ACS
RN 115826-30-7 REGISTRY
CN L-Histidine, L-seryl-glycyl-L-.alpha.-glutamyl-L-tryptophyl-L-valyl-L-methionyl-L-lysyl-L-.alpha.-glutamyl-L-seryl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-threonyl-L-cysteinyl-L-cysteinyl-L-prolyl-L-seryl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl-L-.alpha.-aspartyl-L-isoleucyl-L-threonyl-L-tyrosyl- (9CI) (CA INDEX NAME)
SQL 32
RN 115826-30-7 REGISTRY
SQL 32

SEQ 1 SGEWVMKESR EWKHWVFYTC CPSTPYLDIT YH
======
HITS AT: 12-17

REFERENCE 1: 104:136149

L16 ANSWER 23 OF 25 REGISTRY COPYRIGHT [illegible] ACS
RN 115826-29-4 REGISTRY
CN L-Histidine, L-seryl-glycyl-L-.alpha.-glutamyl-L-tryptophyl-L-valyl-L-methionyl-L-isoleucyl-L-lysyl-L-glutamyl-L-seryl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-cysteinyl-L-prolyl-L-seryl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl-L-.alpha.-aspartyl-L-isoleucyl-L-threonyl-L-tyrosyl- (9CI) (CA INDEX NAME)
SQL 32
RN 115826-29-4 REGISTRY
SQL 32

SEQ 1 SGEWVIKEWA EWKHWVFYAC CPSTPYLDIT YH
[illegible]
HITS AT: 12-17

REFERENCE 1: [illegible]

L16 ANSWER 24 OF 25 REGISTRY COPYRIGHT 2006 ACS
RN 114753-46-7 REGISTRY
CN L-Alanine, L-lysyl-L-.alpha.-glutamyl-L-seryl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl- (9CI) (CA INDEX NAME)
SQL 13
RN 114753-46-7 REGISTRY
SQL 13

SEQ 1 KESRGWKHTV FYA
[illegible]
HITS AT: 6-11

REFERENCE 1: 113:128235

REFERENCE 2: [illegible]

L16 ANSWER 25 OF 25 REGISTRY COPYRIGHT 2006 ACS
RN 89808-58-2 REGISTRY
CN Cyclo(N-methyl-L-alanyl-2-iodo-L-phenylalanyl-D-tryptophyl-L-lysyl-L-valyl-L-tryptophyl) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN 1,4,7,10,13,16-Hexaazacyclooctadecane, cyclic peptide deriv.
CN Cyclo(N-methyl-L-alanyl-2-iodo-L-phenylalanyl-D-tryptophyl-L-lysyl-L-valyl-L-tryptophyl)
NTE cyclic
modified

type	------ location ------		description
modification	Ala-1	-	methyl<Me>
modification	Phe-2	-	iodo<I>

SQL 6
RN 89808-58-2 REGISTRY
SQL 6

SEQ 1 AFWKVW
[illegible]
HITS AT: 1-2, 3-6

REFERENCE 1: [illegible]